(12) NACH DEM VERTRAG ÜBER DIE INTERNATIONALE ZUSAMMENARBEIT AUF DEM GEBIET DES PATENTWESENS (PCT) VERÖFFENTLICHTE INTERNATIONALE ANMELDUNG

(19) Weltorganisation für geistiges Eigentum
Internationales Büro

(43) Internationales Veröffentlichungsdatum
8. März 2001 (08.03.2001)

PCT

(10) Internationale Veröffentlichungsnummer
WO 01/16303 A2

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(54) Title: NUCLEIC ACIDS WHICH CODE FOR THE ENZYME ACTIVITIES OF THE SPINOSYN BIOSYNTHESIS

(54) Bezeichnung: NUCLEINSÄUREN, DIE FÜR ENZYMAKTIVITÄTEN DER SPINOSYN-BIOSYNTHESE CODIEREN

(57) Abstract: The present invention relates to nucleic acids which code for the enzyme activities of the spinosyn biosynthesis. The invention also relates to the corresponding enzymes as such. The invention further relates to a method for producing spinosyn derivatives and spinosyn precursors.

(57) Zusammenfassung: Die vorliegende Erfindung betrifft Nucleinsäuren, die für Enzymaktivitäten der Spinosyn-Biosynthese codieren, sowie die entsprechenden Enzyme per se. Weiterhin betrifft die Erfindung Verfahren zum Herstellen von Spinosyn-Derivaten und -Vorstufen.

Nucleinsäuren, die für Enzymaktivitäten der Spinosyn-Biosynthese codieren

Die vorliegende Erfindung betrifft Nucleinsäuren, die für Enzymaktivitäten der Spinosyn-Biosynthese codieren, sowie die entsprechenden Enzyme per se.

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Spinosyne stellen eine neue Gruppe von makrolidischen Verbindungen dar, die aus dem Actinomyceten *Saccharopolyspora spinosa* isoliert worden sind (Mertz und Yao, 1990). Sie werden zur Bekämpfung von Insekten eingesetzt (WO 97/00265, WO 94/20518, WO 93/09126, US 5670364, US 5362634, US 5227295, US

10   5202242). Spinosyne zeigen eine starke insektizide, jedoch keine antibakterielle Aktivität, wodurch sie von den konventionellen Makroliden, wie Tylosin, Spiramycin und Erythromycin, die keine insektizide, jedoch antimikrobielle Wirksamkeit aufweisen, unterscheidbar sind.

15   Die Struktur der Spinosyne setzt sich zusammen aus einem tetracyclischen Polyketidgrundgerüst (Aglycon) mit einem 12-gliedrigen Makrolidring und einem 5,6,5-cis-anti-trans-Tricyclus, sowie einem D-Forosamin- und einem 2,3,4-Tri-O-Methyl-L-Rhamnose-Zuckeranteil (Kirst et al., 1991). Mehr als 20 verschiedene natürliche Spinosyn-Derivate, der sogenannte A83543 Komplex, ist bisher beschrieben worden

20   (WO 97/00265, WO 94/20518, WO 93/09126). Diese Derivate variieren in der Substitution von einer oder einigen Methylgruppen am tetracyclischen Grundgerüst, am Forosamin- oder am Tri-Methyl-Rhamnose-Zuckeranteil. Ein 17-Pseudoaglycon, dem der Forosamin-Zuckeranteil fehlt, ist ebenfalls aus Kulturbrühen von *S. spinosa* isoliert worden.

25

Die Hauptkomponenten des von *S. spinosa* gebildeten A83543 Komplexes stellen die Varianten Spinosyn A und Spinosyn D dar, die die wesentlichen Bestandteile des Produktes Spinosad darstellen (vgl. Pesticide Manual, British Crop Protection Council, 11th Ed., 1997, Seite 1272 und Dow Elanco trade maganzine Down to Earth,

30   Vol. 52, NO:. 1, 1997 und die darin zitierte Literatur).

Aufbauend auf Untersuchungen zum Einbau von C^{13}-markiertem Acetat, Propionat, Butyrat oder Isobutyrat konnte gezeigt werden, dass die Biosynthese von A83543 einem Polyketid-Biosyntheseweg folgt (Nakatsukasa et al., 1990). Polyketide werden durch multifunktionelle Enzyme, den sog. Polyketidsynthasen (PKS's) aus kurz-

5   kettigen Säurebausteinen wie Acetat, Propionat oder Butyrat aufgebaut. Ähnlich wie die verwandten Fettsäuresynthasen (FAS's) katalysieren sie decarboxylierende Poly-kondensationsschritte der als CoA-Thioester aktivierten Bausteine. Während FAS's nach jedem Kondensationsschritt eine vollständige Reduktion der intermediär an der wachsenden Polyketidkette entstehenden β-Oxoester durch Ketoreduktion, Dehy-

10   dratation und Enoylreduktion katalysieren, können PKS's bestimmte Reduktions-schritte auslassen. Modulare Typ I PKS's bestehen aus einem oder mehreren großen multifunktionalen Proteinen. Iterative Typ II PKS's stellen dagegen einen Komplex aus weitgehend monofunktionalen Proteinen dar.

15   Die enzymatischen Aktivitäten von modularen Typ I PKS's lassen sich zu soge-nannten Modulen zusammenfassen. Hierbei trägt ein Modul eine Anordnung von drei enzymkatalytisch aktiven Domänen, die zu einer Verlängerung der wachsenden Poly-ketidkette um eine biosynthetische Verlängerungseinheit führen. Bei diesen Domänen handelt es sich um eine β-Ketoacyl:Acyl Carrier Protein Synthase-

20   Domäne, eine Acyltransferase-Domäne und eine β-Ketoacyl:Acyl Carrier Protein-Domäne. Ein Modul kann auch eine Ketoreduktase-, eine Dehydratase-, eine Enoyl-reduktase- und eine Thioesterase-Domäne tragen. Ein sog. Ladungsmodul, das am Beginn der Biosynthese steht kann von den genannten Domänen lediglich eine Acyl-transferase-Domäne und eine β-Ketoacyl:Acyl-Carrier Protein-Domäne tragen, sowie

25   eine enzymatisch inaktive β-Ketoacyl:Acyl Carrier Protein Synthase-Domäne. Eine Polyketidsynthase-Domäne umfasst jeweils eine dieser genannten enzymatischen Aktivitäten.

Aufgrund der potenten insektiziden Wirkung sowie der bemerkenswerten Struktur

30   der Spinosyne besteht ein großes Interesse, die genetischen Informationen für deren Biosynthese zu entschlüsseln.

- 3 -

Gegenstand der Erfindung sind Nucleinsäuren, welche zumindest eine Region umfassen, die für eine Enzymaktivität codiert, welche an der Biosynthese von Spinosynen beteiligt ist.

5

Die vorliegende Erfindung stellt ein Cluster von offenen Leserahmen (ORF´s) bereit, deren Translationsprodukte an der Biosynthese von Spinosynen beteiligt sind. Weiterhin werden zusätzliche Gene bzw. ORF´s bereitgestellt, die außerhalb des ca. 120 kb großen Spinosyn-Biosyntheseclusters liegen, und deren Translationsprodukte

10   an der Rhamnose-Zuckerbiosynthese beteiligt sind.

Bei den erfindungsgemäßen Nucleinsäuren handelt es sich insbesondere um einzelsträngige oder doppelsträngige Desoxyribonucleinsäuren (DNA) oder Ribonucleinsäuren (RNA). Bevorzugte Ausführungsformen sind Fragmente genomischer DNA

15   und cDNA´s.

Der Ausdruck "zumindest eine Region", wie er hierin verwendet wird, bedeutet, dass die erfindungsgemäße Nucleinsäure eine oder mehrere Sequenzen umfassen kann, welche jeweils für einzelne Aktivitäten codieren, die Schritte bei der Synthese von

20   Spinosynen durchführen. Es werden demnach auch Nucleinsäuren als erfindungsgemäß betrachtet, die nur für eine einzige Enzymaktivität der Spinosyn-Biosynthese codieren.

Der Ausdruck "Enzymaktivität", wie er hierin verwendet wird, bedeutet, dass

25   ausgehend von den hierin betrachteten Nucleinsäuren zumindest derjenige Teil eines vollständigen Enzyms exprimiert werden kann, der noch die Katalyseeigenschaften des Enzyms ausübt.

Insbesondere codieren die erfindungsgemäßen Nucleinsäuren für Enzymaktivitäten

30   von Polyketidsynthasen, Methyltransferasen, Epimerasen, Glycosyltransferasen,

- 4 -

Aminotransferasen, Dimethyltransferasen, Reduktasen, Dehydratasen und/oder Cyclisierungsenzymen.

Bevorzugt handelt es sich bei den erfindungsgemäßen Nucleinsäuren um DNA-
Fragmente, die genomischer DNA von *S. spinosa* entsprechen.

Besonders bevorzugt umfassen die erfindungsgemäßen Nucleinsäuren zumindest eine Sequenz ausgewählt aus

(a)   den Sequenzen gemäß SEQ ID NOS: 1, 2, 3, 4, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 52 oder 54,

(b)   zumindest 14 Basenpaare langen Teilsequenzen der unter (a) defi-
nierten Sequenzen,

(c)   Sequenzen, welche an die unter (a) definierten Sequenzen hybri-
disieren,

(d)   Sequenzen, welche eine zumindest 70 %ige, bevorzugt eine 80 %ige, besonders bevorzugt eine 90 %ige Identität zu den unter (a) definier-
ten Sequenzen aufweisen,

(e)   Sequenzen, welche zu den unter (a) definierten Sequenzen komple-
mentär sind, und

(f)   Sequenzen, welche aufgrund der Degeneriertheit des genetischen Codes für dieselbe Aminosäuresequenz kodieren wie die unter (a) bis (d) definierten Sequenzen.

- 5 -

Der Ausdruck "hybridisieren", wie er hierin verwendet wird, beschreibt den Vor-
gang, bei welchem ein einzelsträngiges Nucleinsäuremolekül mit einem komple-
mentären Strang eine Basenpaarung eingeht. Auf diese Weise können beispielsweise
ausgehend von genomischer DNA aus Organismen, die phylogenetisch mit *S.*
5   *spinosa* verwandt sind und die Fähigkeit der Biosynthese von Spinosynen besitzen,
DNA-Fragmente isoliert werden, welche dieselben Eigenschaften wie die aus *S.*
spinosa isolierten Fragmente aufweisen.

Bevorzugte Hybridisierungsbedingungen sind nachstehend angegeben: Hybridisie-
10   rungslösung: 5 x SSC; Blocking Reagens (Roche Diagnostics GmbH, Mannheim,
Deutschland), 1 %; N-Lauroylsarcosin, 0,1 %; SDS (Sodiumdodecylsulfate) 0,02 %;
Hybridisierungstemperatur: 60°C; erster Waschschritt: 2 x SSC bei 60°C; zweiter
Waschschritt: 2 x SSC bei 60°C; bevorzugt zweiter Waschschritt: 0,5 x SSC bei
60°C; besonders bevorzugt zweiter Waschschritt: 0,2 x SSC bei 60°C.

15

Der Grad der Identität der Nucleinsäuren wird vorzugsweise bestimmt mit Hilfe des
Programms GAP aus dem Programmpaket GCG (Devereux et al., 1984), Version 9.1
unter Standardeinstellungen.

20   Besonders hervorgehoben werden Nucleinsäuren, die

   (1)   entweder alle Sequenzen, die für Schritte der Forosamin- und Trimethyl-
          Rhamnose-Biosynthese codieren, umfassen, insbesondere die Sequenzen ge-
          mäß SEQ ID NOS: 4 und 51, oder

25   (2)   alle Sequenzen, die für Schritte der Polyketidsynthese codieren, umfassen,
          insbesondere die Sequenzen gemäß SEQ ID NOS: 5 und 6, oder

   (3)   alle Sequenzen, die für alle Schritte der Forosamin-, Trimethyl-Rhamnose-
          und Polyketidsynthese codieren, umfassen, insbesondere die Sequenzen ge-
          mäß SEQ ID NOS: 1, 2, 3 und 51.

30

- 6 -

Alle zur Spinosyn-Biosynthese oder zur Synthese von Vorstufen, wie sie nachstehend definiert sind, benötigten DNA-Sequenzen können sich somit auf einem einzelnen Vektor befinden. Diese Nucleinsäuren können aber auch auf zwei oder mehreren Vektoren vorliegen und gleichzeitig oder nacheinander in einer Wirtszelle

5   exprimiert werden.

Alle ORF's der erfindungsgemäßen Nucleinsäuren können von ihren eigenen Promotoren oder von heterologen Promotoren angeschaltet werden.

10   Gegenstand der vorliegenden Erfindung sind auch die regulatorischen Regionen, welche natürlicherweise, d.h. im Ursprungsorganismus *S. spinosa*, die Transkription der erfindungsgemäßen Nucleinsäuren kontrollieren.

Der Ausdruck "regulatorische Regionen", wie er hierin verwendet wird, bezieht sich

15   auf Promotoren, Repressor- oder Aktivator-Bindungsstellen, Repressor- oder Aktivatorsequenzen, und Terminatoren. Ferner sind genetisch mobile Elemente, welche natürlicherweise, d.h. im Ursprungsorganismus *S. spinosa* vorkommen, ebenfalls von diesem Ausdruck umfasst. Solche genetisch mobilen Elemente können transposable oder mobilisierbare Elemente oder funktionelle Teile davon, IS-Elemente oder an-

20   dere Insertionselemente sein. Weiterhin sind auch amplifizierbare DNA-Elemente (Amplifiable Units of DNA, AUD; Fishman and Hershberger, 1983), welche natürlicherweise, d.h. im Ursprungsorganismus *S. spinosa* vorkommen, von diesem Ausdruck umfasst. Die Erfindung betrifft auch jede Kombination dieser regulatorischen Regionen untereinander oder mit heterologen DNA-Fragmenten, wie z.B. Promo-

25   toren, Repressor oder Aktivator-Bindungsstellen, transposablen, mobilisierbaren oder transduzierbaren Elementen.

Gegenstand der vorliegenden Erfindung sind weiterhin DNA-Konstrukte, die zumindest eine erfindungsgemäße Nucleinsäure und einen heterologen Promotor um-

30   fassen.

Der Ausdruck "heterologer Promotor", wie er hierin verwendet wird, bezieht sich auf einen Promotor, der im Ursprungsorganismus nicht die Expression des betreffenden Gens (ORF's) kontrolliert.

5   Die Auswahl von heterologen Promotoren ist davon abhängig, ob zur Expression pro- oder eukaryotische Zellen oder zellfreie Systeme verwendet werden. Ein bevorzugtes Beispiele für einen heterologen Promotor ist der Promotor des *mel*-Gens aus dem Vektor pIJ702 (The John Innes Foundation, Norwich, UK 1985). Die heterologe Expression kann z.B. eingesetzt werden, um zu einer Steigerung der Produktion von

10   Spinosyn im Vergleich zum natürlichen Spinosyn-Produzenten zu gelangen.

Gegenstand der Erfindung sind ferner Vektoren, die zumindest eine der erfindungsgemäßen Nucleinsäuren enthalten. Als Vektoren können alle in molekularbiologischen Laboratorien verwendeten Phagen, Plasmide, Phagmide, Phasmide,

15   Cosmide, YACs, BACs, PACs, künstliche Chromosomen oder Partikel, die für einen Partikelbeschuss geeignet sind, verwendet werden.

Bevorzugt sind BAC-Vektoren. BAC-Vektoren (Bacterial Artificial Chromosome) sind entwickelt worden zur Klonierung von großen DNA-Fragmenten (Shizuya et al.,

20   1992). Es handelt sich um "single-copy" Plasmide mit einem F-Faktor Origin, die DNA-Fragmente mit einer durchschnittlichen Größe von 120 Kilobasenpaaren (kb) tragen können. Sie sind replizierbar in *Escherichia coli*. Der BAC-Vektor pBeloBAC11 (Kim et al., 1996) trägt einen T7 und einen SP6 Promotor, welche die Klonierungsstelle flankieren und als Startbereich für Sequenzierungsprimer sowie

25   zur Generierung von RNA-Transkripten verwendet werden können.

Besonders bevorzugt sind die am 18. August 1999 bei der Deutschen Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), Mascheroder Weg 1b, D-38124 Braunschweig, in Übereinstimmung mit den Bestimmungen des Budapester Ver-

30   trages unter den Hinterlegungsnummern DSM 13010, DSM 13011 und DSM 13012 hinterlegten BAC-Shuttleklone, die Gegenstand der vorliegenden Erfindung sind.

- 8 -

Die hinterlegten BAC-Shuttleklone P11/G6, P8/G11 und P11/B10 tragen jeweils ein mindestens 100 kb großes DNA-Fragment aus *S. spinosa*. Die Klone P11/G6 und P11/B10 tragen jeweils einen Teil der Nucleinsäuresequenz gemäß SEQ ID NO: 4, sowie die angrenzenden vollständigen Nucleinsäuresequenzen gemäß SEQ ID NOS: 5 und 6, sowie einen an die Nucleotidsequenz gemäß SEQ ID NO: 6 3′angrenzende DNA-Bereich (Abb. 7). Der Klon P8/G11 trägt einen Teil der Nucleinsäuresequenz gemäß SEQ ID NO: 6, die vollständigen Nucleinsäuresequenzen gemäß SEQ ID NOS: 5 und 4, sowie einen an die Sequenz gemäß SEQ ID NO: 4 3′-angrenzenden DNA-Bereich (Abb. 7).

In gleicher Weise sind auch PAC- und alle anderen funktionell gleichwertigen Vektoren, die es erlauben, große DNA-Fragmente, insbesondere solche DNA-Fragmente, die größer als 30 kb, vorzugsweise größer als 40 kb, besonders bevorzugt größer als 60 kb sind, in heterologe Wirtszellen zu übertragen und dort eine Etablierung von Fremd-DNA zu gewährleisten, für eine Spinosyn-Produktion ge-eignet. Vorzugsweise werden solche BAC-, PAC- und funktionell gleichwertigen Vektoren verwendet, die zu einem Shuttle-Vektor modifiziert sind und z.B. eine Plasmidreplikation sowohl in Gram-negativen Bakterien, wie *Escherichia coli*, als auch in Gram-positiven Bakterien, wie *Streptomyces*, erlauben. Solche bevorzugten Shuttle-Vektoren können DNA-Fragmente einer Größe tragen, die in üblichen Vektoren, wie z.B. Cosmidvektoren, nicht klonierbar sind und nicht in heterologe Wirte, wie Actinomyceten, z.B. Streptomyceten, übertragbar sind. Letztere Vektoren können sowohl durch Transformation, Konjugation, Elektroporation, Protoplasten-transformation oder andere geeignete Verfahren übertragen werden. In hervor-ragender Weise sind solche Shuttle-Vektoren innerhalb einer heterologen Population Gram-negativer oder Gram-positiver Bakterien, zwischen Gram-positiven und Gram-negativen Bakterien, zwischen Bakterien und Archea, zwischen Pro- und Eukaryonten konjugativ übertragbar. Die in heterologe Wirte, wie z.B. Streptomyceten, übertragenen BAC-, PAC- oder funktionell gleichwertigen Shuttle-Vektoren können autonom repliziert werden oder ins Genom des Wirtes integriert

- 9 -

werden. Letztere Integration kann über homologe Rekombination, über einen ΦC31-Integrationsmechanismus (Hopwood et al., 1985), über ortsspezifische Integration, die von pSAM2 (Smokvina et al., 1990; WO 95/16046) determinierten Funktionen abhängt oder über Mini-Circle vermittelte Funktionen (Motamedi et al., 1995;
5   WO 96/00282) erfolgen.

Solche Shuttle-Vektoren erlauben es, spezifische, durch außerordentlich große DNA-Bereiche determinierte Biosynthesewege von Primär- oder Sekundärmetaboliten, durch Transfer eines einzigen rekombinanten Vektors heterolog in besonders ge-
10   eigneten Wirtszellen zu exprimieren. So kann das identifizierte Cluster für die Bio-synthese von Spinosyn in Organismen, wie Actinomyceten, z.B. *Streptomyces*, durch Transfer eines einzigen rekombinanten Shuttle-Vektors ausgeprägt werden. Aufgrund der Größe dieses Biosyntheseclusters ist diese heterologe Expression der Spinosyn-Biosynthese mit einem einzigen Cosmidvektor nicht möglich. Die Übertragung eines
15   rekombinanten BAC-, PAC- oder funktionell gleichwertigen Shuttle-Vektors, der die erfindungsgemäßen Nucleinsäuren trägt, kann zu einer signifikanten Steigerung der Produktion von Spinosyn im Vergleich zur Spinosyn-Produktion des Stammes *S. spinosa* oder abgeleiteter Mutanten mit erhöhter Spinosyn-Bildung führen. Zudem kann ein solcher, für die Spinosyn-Biosynthese codierender Shuttle-Vektor genutzt
20   werden, um nach Übertragung in heterologe Wirtszellen deren Biosynthese- und Modifizierungsleistung auszunutzen, um zu einer signifikanten Modifizierung von Spinosyn oder Spinosyn-Biosynthesevorstufen zu gelangen. Hierdurch ist es zudem möglich, neue Spinosyn-Derivate durch den Transfer eines einzigen rekombinanten Vektors in heterologe Wirtszellen herzustellen.

25

Weiterhin können solche Shuttle-Vektoren verwendet werden, klonierte Biosynthese-wege von Sekundärmetaboliten als Bestandteil eines einzigen rekombinanten Shuttle-Vektors genetisch zu modifizieren. Solche Modifizierungen können z.B. in einem *E. coli* Wirt durchgeführt werden, z.B. unter Ausnutzung von Re-
30   kombinationsereignissen unter Beteiligung des recA-Genproduktes oder der recE-und recT-Genprodukte (Muyrers et al., 1999). Weiterhin können solche Vektoren

durch *in vitro*-Verfahren, wie z.B. das Template Generation System (Finnzymes, FIN-02201, Espoo, Finnland) oder das Transposomics-System (Epicentre Technologies, Biozym Diagnostika GmbH, Oldendorf, Deutschland) modifiziert werden. Solche, für veränderte Biosynthesewege codierende Shuttle-Vektoren können dann in geeignete Wirtszellen übertragen werden, um zur Produktion veränderter Sekundärmetabolite zu gelangen. In analoger Weise können die genannten Shuttle-Vektoren genutzt werden, die erfindungsgemäßen Nucleinsäuren zu modifizieren, um sie dann, nach Transfer in geeignete Wirtszellen zur Produktion veränderter Spinosyne einzusetzen.

Teile der erfindungsgemäßen Nucleinsäuren können auch als Bestandteil von zwei oder mehreren Vektoren, wie z.B. Cosmidvektoren, eine genetische Information determinieren, die in Kombination miteinander zur Biosynthese von Spinosyn oder Spinosyn-Vorstufen, wie z.B. Pseudoaglycon oder Spinosyn-Aglycon geeignet sind. Solche Kombinationen von rekombinanten Vektoren können eingesetzt werden, um zu einer Spinosyn-Produktion in anderen Organismen als *S. spinosa* zu gelangen. Dies kann bei einer Expression in besonders geeigneten Wirten zu einer signifikanten Steigerung der Spinosyn-Produktion im Vergleich zu *S. spinosa* oder abgeleiteten produktionsverstärkten Mutanten führen. Weiterhin ist es möglich, erfindungsgemäße Nucleinsäuren in einzelnen rekombinanten Vektoren dieser Vektorkombination so zu verändern, dass eine heterologe Produktion von Spinosyn-Derivaten in Wirtszellen möglich ist. Desweiteren kann eine solche Kombination von rekombinanten Vektoren durch deren Transfer in heterologe Wirte zur Bildung neuer Spinosyn-Derivate unter Ausnutzung des wirtseigenen Enzymsystems geeignet sein.

Gegenstand der vorliegenden Erfindung sind auch Wirtszellen, die zumindest eine der erfindungsgemäßen Nucleinsäuren enthalten. Als Wirtszelle eignen sich sowohl prokaryotische Zellen, vorzugsweise Actinomyceten, besonders bevorzugt Streptomyceten, als auch eukaryotische Zellen, wie Säugerzellen, Pflanzenzellen oder Hefezellen.

- 11 -

In besonderer Weise können die erfindungsgemäßen Nucleinsäuren in pflanzliche Zellen übertragen und exprimiert werden. Hierdurch können transgene Pflanzen hergestellt werden, die das pflanzenschützende, insektizide Spinosyn bzw. Derivate davon produzieren. Eine Übertragung der erfindungsgemäßen Nucleinsäuren in die
5   Pflanzenzellen oder pflanzliche Zellkulturen kann mit üblichen Verfahren u.a. auch durch Partikelbeschuss erfolgen.

Gegenstand der vorliegenden Erfindung sind weiterhin die Polypeptide, die von den erfindungsgemäßen Nucleinsäuren codiert werden. Die erfindungsgemäßen Poly-
10   peptide können ein vollständiges Enzym darstellen, das einen Schritt der Spinosyn-Biosynthese katalysiert. Jedoch sind auch solche Polypeptide von der Erfindung erfasst, die nur einen Teil der vollständigen Aminosäuresequenz des betreffenden Enzyms aufweisen.

15   Der Ausdruck "Teilsequenz", wie er hierin verwendet wird, bezieht sich somit auf die Aminosäuresequenz eines Polypeptids, das noch die Aktivität des entsprechenden vollständigen Enzyms oder einer enzymatisch aktiven Domäne ausüben kann.

Im Folgenden werden bevorzugte erfindungsgemäße Nucleinsäuren und Polypeptide
20   mit Bezug auf die entsprechenden SEQ ID NOS näher charakterisiert.

SEQ ID NOS: 7 und 8, ORF1:
Nucleotidpositon 828 bis 1 der SEQ ID NO: 4, 275 Aminosäuren;
das ableitbare Genprodukt ist eine Methyltransferase.

25

SEQ ID NOS: 9 und 10, ORF2:
Nucleotidposition 1.283 bis 2.455 der SEQ ID NO: 4, 390 Aminosäuren;
das ableitbare Genprodukt ist eine Glycosyltransferase.

- 12 -

SEQ ID NOS: 11 und 12, ORF3:

Nucleotidposition 2.495 bis 3.247 der SEQ ID NO: 4, 250 Aminosäuren;

das ableitbare Genprodukt ist eine Methyltransferase.

5   SEQ ID NOS: 13 und 14, ORF4:

Nucleotidposition 4.440 bis 3.253 der SEQ ID NO: 4, 395 Aminosäuren;

das ableitbare Genprodukt ist eine Methyltransferase.

SEQ ID NOS: 15 und 16, ORF5:

10   Nucleotidposition 4.578 bis 6.197 der SEQ ID NO: 4, 539 Aminosäuren;

das ableitbare Genprodukt ist ein C-C verknüpfendes Enzym, das Cyclisierungs-
reaktionen durchführt.

SEQ ID NOS: 17 und 18, ORF6:

15   Nucleotidposition 6.211 bis 7.404 der SEQ ID NO: 4, 397 Aminosäuren;

das ableitbare Genprodukt ist eine Methyltransferase.

SEQ ID NOS: 19 und 20, ORF7:

Nucleotidposition 7.401 bis 8.300 der SEQ ID NO: 4, 299 Aminosäuren;

20   das ableitbare Genprodukt ist eine Methyltransferase.

SEQ ID NOS: 21 und 22, ORF8:

Nucleotidposition 8.300 bis 9.466 der SEQ ID NO: 4, 388 Aminosäuren;

das ableitbare Genprodukt ist ein Enzym, das an Cyclisierungsreaktionen beteiligt ist.

25

SEQ ID NOS: 23 und 24, ORF9:

Nucleotidposition 10.572 bis 9.562 der SEQ ID NO: 4, 336 Aminosäuren.

das ableitbare Genprodukt ist eine 2,3-Reduktase.

SEQ ID NOS: 25 und 26, ORF10:

Nucleotidposition 12.029 bis 10.569 der SEQ ID NO: 4, 486 Aminosäuren;

das ableitbare Genprodukt ist eine 2,3-Dehydratase.

5   SEQ ID NOS: 27 und 28, ORF11:

Nucleotidposition 12.549 bis 12.109 der SEQ ID NO: 4, 146 Aminosäuren; das

ableitbare Genprodukt hat Homologien zu einer Thioesterase.

SEQ ID NOS: 29 und 30, ORF12:

10   Nucleotidposition 13.865 bis 12.546 der SEQ ID NO: 4, 439 Aminosäuren;

das ableitbare Genprodukt ist eine Glykosyltransferase.

SEQ ID NOS: 31 und 32, ORF13:

Nucleotidposition 14.245 bis 15.633 der SEQ ID NO: 4, 462 Aminosäuren;

15   das ableitbare Genprodukt ist eine 3,4-Dehydratase.

SEQ ID NOS: 33 und 34, ORF14:

Nucleotidposition 15.671 bis 16828 der SEQ ID NO: 4, 385 Aminosäuren;

das ableitbare Genprodukt ist eine 4-Aminotransferase.

20

SEQ ID NO: 35 und 36, ORF15:

Nucleotidposition 16.831 bis 17.580 der SEQ ID NO: 4, 249 Aminosäuren;

das ableitbare Genprodukt ist eine N-Dimethyltransferase.

25   SEQ ID NOS: 37 und 38, ORF16:

Nucleotidposition 18.930 bis 18.205 der SEQ ID NO: 4, 241 Aminosäuren;

das ableitbare Genprodukt ist eine 3,4-Reduktase.

SEQ ID NOS: 39 und 40, ORF17:

30   Nucleotidposition 19.025-19.861 der SEQ ID NO: 4, 278 Aminosäuren;

das ableitbare Genprodukt ist ein Transkriptions-Regulator.

- 14 -

SEQ ID NOS: 41 und 42, ORF18:

 Nucleotidpositionen 116-7903 der SEQ ID NO: 5, Aminosäurepositionen 1 bis
2595:

5   Nucleotidpositionen 128-1402, Aminosäure Positionen 5-429 codieren eine β-
Ketoacyl:Acyl Carrier Protein Synthase-Domäne;

Nucleotidpositionen 1691-2656, Aminosäurepositionen 526-847 codieren eine
Acyltransferase-Domäne;

Nucleotidpositionen 2798-3052, Aminosäurepositionen 895-979 codieren eine β-

10   Ketoacyl:Acyl Carrier Protein-Domäne;

Nucleotidpositionen 3107-4372, Aminosäurepositionen 998-1419 codieren eine β-
Ketoacyl:Acyl Carrier Protein Synthase-Domäne;

Nucleotidpositionen 4688-5662, Aminosäurepositionen 1525-1849 codieren eine
Acyltransferase-Domäne;

15   Nucleotidpositionen 6587-7138, Aminosäurepositionen 2158-2341 codieren eine
Ketoreduktase-Domäne;

Nucleotidpositionen 7409-7666, Aminosäurepositionen 2432-2517 codieren eine β-
Ketoacyl:Acyl Carrier Protein-Domäne.

20   SEQ ID NOS: 43 und 44, ORF19:

Nucleotidpositionen 7921-14379 der SEQ ID NO: 5, Aminosäurepositionen 1 bis
2152:

Nucleotidpositionen 8029-9318, Aminosäurepositionen 37-466 codieren eine β-
Ketoacyl:Acyl Carrier Protein Synthase-Domäne;

25   Nucleotidpositionen 9634-10608, Aminosäurepositionen 572-896 codieren eine
Acyltransferase-Domäne;

Nucleotidpositionen 10705-11259, Aminosäurepositionen 929-1113 codieren eine
Dehydratase-Domäne;

Nucleotidpositionen 12043-13080, Aminosäurepositionen 1375-1720 codieren eine

30   Enoylreduktase-Domäne;

- 15 -

Nucleotidpositionen 13093-13635, Aminosäurepositionen 1725-1905 codieren eine Ketoreduktase-Domäne;

Nucleotidpositionen 13885-14142, Aminosäurepositionen 1989-2074 codieren eine β-Ketoacyl:Acyl Carrier Protein-Domäne.

5

SEQ ID NOS: 45 und 46, ORF20:

Nucleotidpositionen 14424-23936 der SEQ ID NO: 5, Aminosäurepositionen 1 bis 3170:

Nucleotidpositionen 14523-15824, Aminosäurepositionen 34-467 codieren eine β-

10   Ketoacyl:Acyl Carrier Protein Synthase-Domäne;

Nucleotidpositionen 16110-17075, Aminosäurepositionen 563-884 codieren eine Acyltransferase-Domäne;

Nucleotidpositionen 17997-18536, Aminosäurepositionen 1192-1371 codieren eine Ketoreduktase-Domäne;

15   Nucleotidpositionen 18795-19052, Aminosäurepositionen 1458-1543 codieren eine β-Ketoacyl:Acyl Carrier Protein-Domäne;

Nucleotidpositionen 19107-20387, Aminosäurepositionen 1562-1988 codieren eine β-Ketoacyl:Acyl Carrier Protein Synthase-Domäne;

Nucleotidpositionen 20718-21692, Aminosäurepositionen 2099-2423 codieren eine

20   Acyltransferase-Domäne;

Nucleotidpositionen 22620-23171, Aminosäurepositionen 2733-2916 codieren eine Ketoreduktase-Domäne;

Nucleotidpositionen 23436-23693, Aminosäurepositionen 3005-3090 codieren eine β-Ketoacyl:Acyl Carrier Protein-Domäne.

25

SEQ ID NOS: 47 und 48, ORF21:

Nucleotidpositionen 23983-38757 der SEQ ID NO: 5, Aminosäurepositionen 1 bis 4924:

Nucleotidpositionen 24082-25392, Aminosäurepositionen 34-470 codieren eine β-

30   Ketoacyl:Acyl Carrier Protein Synthase-Domäne;

Nucleotidpositionen 25696-26661, Aminosäurepositionen 572-893 codieren eine
Acyltransferase-Domäne;

Nucleotidpositionen 26761-27315, Aminosäurepositionen 927-1111 codieren eine
Dehydratase-Domäne;

5   Nucleotidpositionen 28231-28782, Aminosäurepositionen 1417-1600 codieren eine
Ketoreduktase-Domäne;

Nucleotidpositionen 29035-29265, Aminosäurepositionen 1685-1761 codieren eine
β-Ketoacyl:Acyl Carrier Protein-Domäne;

Nucleotidpositionen 29329-30624, Aminosäurepositionen 1783-2214 codieren eine

10   β-Ketoacyl:Acyl Carrier Protein Synthase-Domäne;

Nucleotidpositionen 30928-31902, Aminosäurepositionen 2316-2640 codieren eine
Acyltransferase-Domäne;

Nucleotidpositionen 32827-33378, Aminosäurepositionen 2949-3132 codieren eine
Ketoreduktase-Domäne;

15   Nucleotidpositionen 33652-33900, Aminosäurepositionen 3224-3306 codieren eine
β-Ketoacyl:Acyl Carrier Protein-Domäne;

Nucleotidpositionen 33952-35262, Aminosäurepositionen 3324-3760 codieren eine
β-Ketoacyl:Acyl Carrier Protein Synthase-Domäne;

Nucleotidpositionen 35554-36522, Aminosäurepositionen 3858-4180 codieren eine

20   Acyltransferase-Domäne;

Nucleotidpositionen 37453-37998, Aminosäurepositionen 4491-4672 codieren eine
Ketoreduktase-Domäne;

Nucleotidpositionen 38254-38511, Aminosäurepositionen 4758-4843 codieren eine
β-Ketoacyl:Acyl Carrier Protein-Domäne.

25

SEQ ID NOS: 49 und 50, ORF22:

Nucleotidpositionen 38808-50000 der SEQ ID NO: 5 und die Nukleotidpositionen 1
bis 5574 der SEQ ID NO: 6, Aminosäurepositionen 1 bis 5588:

Nucleotidpositionen 38907-40226 der SEQ ID NO: 5, Aminosäurepositionen 34-473

30   codiert eine β-Ketoacyl:Acyl Carrier Protein Synthase-Domäne;

- 17 -

Nucleotidpositionen 40494-41453 der SEQ ID NO: 5, Aminosäurepositionen 563-882 codieren eine Acyltransferase-Domäne;

Nucleotidpositionen 41556-42119 der SEQ ID NO: 5, Aminosäurepositionen 917-1104 codieren eine Dehydratase-Domäne;

5   Nucleotidpositionen 43017-43568 der SEQ ID NO: 5, Aminosäurepositionen 1404-1587 codieren eine Ketoreduktase-Domäne;

Nucleotidpositionen 43833-44090 der SEQ ID NO: 5, Aminosäurepositionen 1676-1761 codieren eine β-Ketoacyl:Acyl-Carrier Protein Domäne;

Nucleotidpositionen 44151-45473 der SEQ ID NO: 5, Aminosäurepositionen 1782-

10   2222 codieren eine β-Ketoacyl:Acyl Carrier Protein Synthase-Domäne;

Nucleotidpositionen 45765-46730 der SEQ ID NO: 5, Aminosäurepositionen 2320-2641 codieren eine Acyltransferase-Domäne;

Nucleotidpositionen 46827-47459 der SEQ ID NO: 5, Aminosäurepositionen 2674-2884 codieren eine Dehydratase-Domäne;

15   Nucleotidpositionen 48378-48935 der SEQ ID NO: 5, Aminosäurepositionen 3191-3376 codieren eine Ketoreduktase-Domäne;

Nucleotidpositionen 49182-49412 der SEQ ID NO: 5, Aminosäurepositionen 3459-3535 codieren eine β-Ketoacyl:Acyl Carrier Protein-Domäne;

Nucleotidpositionen 49482-50000 der SEQ ID NO: 5 und Nucleotidposition 1 bis

20   759 der SEQ ID NO: 6, Aminosäurepositionen 3559-3984 codieren eine β-Ketoacyl:Acyl Carrier Protein Synthase-Domäne;

Nucleotidpositionen 1084-2049 der SEQ ID NO: 6, Aminosäurepositionen 4093-4414 codieren eine Acyltransferase-Domäne;

Nucleotidpositionen 2146-2697 der SEQ ID NO: 6, Aminosäurepositionen 4447-

25   4630 codieren eine Dehydratase-Domäne;

Nucleotidpositionen 3604-4155 der SEQ ID NO: 6, Aminosäurepositionen 4933-5116 codieren eine Ketoreduktase-Domäne;

Nucleotidpositionen 4420-4677 der SEQ ID NO: 6, Aminosäurepositionen 5205-5290 codieren eine β-Ketoacyl:Acyl Carrier Protein-Domäne;

30   Nucleotidpositionen 4864-5538 der SEQ ID NO: 6, Aminosäurepositionen 5353-5577 codieren eine Thioesterase-Domäne.

- 18 -

SEQ ID NOS: 52 und 53, ORF23:

Nucleotidposition 344 bis 1333 der SEQ ID NO: 51, 329 Aminosäuren;

das ableitbare Genprodukt ist eine dNDP-Glucose-4,6-Dehydratase.

5

SEQ ID NOS: 54 und 55, ORF24:

Nucleotidposition 1330 bis 2247 der SEQ ID NO: 51, 305 Aminosäuren;

das ableitbare Genprodukt ist eine dNDP-4-keto-6-Deoxyglucose-3,5-Epimerase.

10   Die an der Cyclisierung des 5, 6, 5- Tricyclus beteiligten Produkte des ORF 5 (SEQ
        ID NO: 16) und des ORF 8 (SEQ ID NO: 22) sind aufgrund der ungewöhnlichen
        Cyclisierungsreaktionen von besonderem Interesse. Daher beinhaltet die vorliegende
        Erfindung insbesondere auch homologe Nucleinsäuren oder homologe Genprodukte.
        Vorzugsweise zeigen diese homologen Genprodukte mindestens eine 50 %ige,
15   bevorzugt eine 60 %ige und besonders bevorzugt eine 70 %ige Identität auf Amino-
        säureebene.

        Weiterhin sind Antikörper Gegenstand der Erfindung, die spezifisch an die
        vorstehend genannten Polypeptide binden. Die Herstellung solcher Antikörper erfolgt
20   auf die übliche Weise. Diese Antikörper können genutzt werden, um Expres-
        sionsklone z.B. einer Genbank zu identifizieren, die die erfindungsgemäßen Nuclein-
        säuren tragen.

        Gegenstand der vorliegenden Erfindung sind auch Verfahren zum Herstellen der
25   erfindungsgemäßen Nucleinsäuren. Die erfindungsgemäßen Nucleinsäuren können
        auf die übliche Weise hergestellt werden. Beispielsweise können die Nucleinsäure-
        moleküle vollständig chemisch synthetisiert werden. Man kann auch kurze Stücke
        der erfindungsgemäßen Nucleinsäuren chemisch synthetisieren und solche
        Oligonucleotide radioaktiv oder mit einem Fluoreszenzfarbstoff markieren. Die
30   markierten Oligonucleotide können auch verwendet werden, um Genbanken von
        Organismen zu durchsuchen. Klone, an die die markierten Oligonucleotide hybridi-

sieren, werden zur Isolierung der betreffenden DNA ausgewählt. Nach der Charak-
terisierung der isolierten DNA erhält man auf einfache Weise die erfindungsgemäßen
Nucleinsäuren. Die erfindungsgemäßen Nucleinsäuren können auch mittels PCR-
Verfahren unter Verwendung chemisch synthetischer Oligonucleotide hergestellt
werden.

Gegenstand der vorliegenden Erfindung sind weiterhin Verfahren zum Herstellen der
erfindungsgemäßen Polypeptide. Zur Herstellung der Polypeptide, die von den erfin-
dungsgemäßen Nucleinsäuren codiert werden, können Wirtszellen, die zumindest
eine der erfindungsgemäßen Nucleinsäuren enthalten, unter geeigneten Bedingungen
kultiviert werden. Die gewünschten Polypeptide können danach auf übliche Weise
aus den Zellen oder dem Kulturmedium isoliert werden. Die Polypeptide können
auch in *in vitro*-Systemen hergestellt werden.

Das isolierte und charakterisierte Gencluster und benachbarte oder assoziierte DNA-
Regionen stellen ein Target zur Steigerung der Spinosyn-Biosynthese durch
genetische Manipulation, Über- oder Unterexpression von direkt oder indirekt an der
Biosynthese involvierten Genen oder regulatorischen Sequenzen dar. Diese Mani-
pulationen können sowohl in natürlichen Spinosyn-produzierenden Organismen als
auch in gentechnisch hergestellten Spinosyn-produzierenden Organismen durchge-
führt werden. Beispielsweise können ausgewählte ORF's unter die Kontrolle üblicher
starker Promotoren wie dem *mel*-Promotor des Plasmides pIJ702 (John Innes
Foundation, Norwich, UK, 1985) gestellt werden.

Durch die Klonierung und Identifizierung der Spinosyn-Biosynthesegene schafft die
vorliegende Erfindung die genetische Basis, mittels molekulargenetischer Verfahren
neue Spinosyn-Vorstufen und -Derivate herzustellen.

Der Ausdruck "Spinosyn-Vorstufen", wie er hierin verwendet wird, bezieht sich auf
alle nachweisbaren und alle postulierbaren Biosynthesevorstufen von Spinosyn.

Der Ausdruck "Spinosyn-Derivate", wie er hierin verwendet wird, bezieht sich auf Strukturderivate aller bisher bekannten Spinosyne.

Gegenstand der vorliegenden Erfindung ist somit auch ein Verfahren zum Herstellen von Spinosyn-Vorstufen und -Derivaten.

Die erfindungsgemäßen Nucleinsäuren können beispielsweise eingesetzt werden, um durch kombinatorische Biosynthese neue Spinosyn-Derivate mit Veränderungen des Spinosyn-Aglycons herzustellen. Dies kann z.B. dadurch erreicht werden, dass die von ORF 19 codierte, eine Acetat-Einheit einbauende Acyltransferase-Domäne ausgetauscht wird gegen eine Acyltransferase-Domäne, die eine Propionat-Einheit einbaut. In gleicher Weise kann die, eine Acetat-Einheit einbauende Acyltransferase-Domäne des ORF 18 gegen eine Acyltransferase-Domäne ausgetauscht werden, die eine Propionat-Einheit einbaut. Ferner ist es möglich beide oder jeweils eine Ketoreduktase-Domäne, die von beiden genannten ORF's codiert werden zu inaktivieren, durch eine inaktive Ketoreduktase-Domäne zu ersetzen oder zu deletieren, wodurch eine Hydroxygruppe an der entsprechenden Position im Makrocyclus biosynthetisch hergestellt werden kann. Alle Acyltransferase-, Ketoreduktase-, Dehydratase-, Enoylreduktase-, β-Ketoacyl:Acyl Carrier Protein und Thioesterase-Domänen können einzeln oder in beliebiger Kombination durch entsprechende Polyketidsynthase-Domänen mit anderer Substrat- oder Reaktionsspezifität ersetzt werden, in beliebiger Kombination miteinander fusioniert, einzeln oder in beliebiger Kombination mutagenisiert, deletiert oder dupliziert werden. Ferner können Modulcodierende Sequenzen ausgetauscht werden. So ist es denkbar die Modul 2-codierende DNA-Sequenz (Abb. 6) gegen die Modul 1- oder Modul 3, 4, 5, 6, 7, 8- oder Modul 9-codierende DNA-Sequenz (Abb. 6) zu ersetzen und funktionell zu exprimieren. Es ist auch denkbar die Modul 2-codierende DNA-Sequenz oder jede andere Modul-codierende DNA-Sequenz des Spinosyn-Polyketidsynthase-Genclusters gegen eine andere Modul-codierende DNA-Sequenz des Spinosyn-Polyketidsynthase-Genclusters, die eine andere biosynthetische Verlängerungseinheit einbaut, auszutauschen. Darüber hinaus kann jede andere Modul-codierende DNA-

Sequenz des Spinosyn-Polyketidsynthase-Genclusters gegen eine andere Modul-codierende DNA-Sequenz einer anderen Polyketidsynthase-Nukleinsäuresequenz aus *S. spinosa* oder einem anderen Organismus als *S. spinosa*, wie z.B. *Saccharopolyspora erythraea*, ausgetauscht werden. Diese Veränderungen können

5   unter Ausnutzung der ET-Rekombination (WO 99/29837; Muyrers et al., 1999) oder anderer Klonierungs- und Rekombinationstechniken durchgeführt werden.

Gegenstand der Erfindung sind somit auch alle Modul- oder Domänen-codierenden Nucleinsäuren, die natürlicher oder gentechnisch erzeugter Bestandteil der Spinosyn-

10 Polyketidsynthase sind.

Der Ausdruck "Modul", sowie er hierin verwendet wird, bedeutet, dass eine Anordnung von drei enzymkatalytisch aktiven Domänen vorliegt, die zu eine Verlängerung der wachsenden Polyketidkette um eine biosynthetische Verlängerungseinheit

15 führen. Bei diesen Domänen handelt es sich um eine β-Ketoacyl:Acyl Carrier Protein Synthase-Domäne, eine Acyltransferase-Domäne und eine β-Ketoacyl:Acyl-Carrier Protein-Domäne. Ein Modul kann auch eine Ketoreduktase-, eine Dehydratase-, eine Enoylreduktase- und eine Thioesterase-Domäne tragen. Ein sog. Ladungsmodul, das am Beginn der Biosynthese steht kann von den genannten Domänen lediglich eine

20 Acyltransferase-Domäne und eine β-Ketoacyl:Acyl-Carrier Protein-Domäne tragen, sowie eine enzymatisch inaktive β-Ketoacyl:Acyl Carrier Protein Synthase-Domäne. Eine Polyketidsynthase-Domäne umfasst jeweils eine dieser genannten enzymatischen Aktivitäten.

25 Die erfindungsgemäßen Nucleinsäuren können weiterhin genutzt werden, um im Zuge einer kombinatorischen Biosynthese durch Neuanordnung und Expression von Spinosyn-Polyketidsynthase-Nucleinsäuresequenzen oder durch Kombination und Expression zusammen mit Polyketidsynthase-Nucleinsäuresequenzen einer anderen Polyketidsynthase codierenden Nucleinsäuresequenz aus *S. spinosa* oder einem

30 anderen Organismus, wie z.B. *Saccharopolyspora erythaea*, Bibliotheken von re-kombinanten Polyketidsynthase-Nucleinsäuresequenzen, rekombinanten Polyketid-

- 22 -

synthase-Proteinen oder rekombinant erzeugten Polyketiden herzustellen. Diese Polyketide können durch die Verwendung der erfindungsgemäßen Nucleinsäuren oder die Verwendung anderer Nucleinsäuren, deren ableitbaren Produkte an der Biosynthese anderer Zucker und Ankopplung ans Aglycon beteiligt sind, glycosyliert werden. Es ist bekannt, dass die Glycosylierung des Aglycons eine entscheidende Rolle bei der biologischen Aktivtät am Wirkort spielt. Diese Veränderungen können sowohl in natürlichen als auch in gentechnisch hergestellten Spinosyn-produzierenden Organismen, insbesonders Bakterien, erfolgen. Weiterhin können diese Veränderungen unter Ausnutzung der ET-Rekombination (WO 99/29837; Muyrers et al., 1999) oder anderer Klonierungs- und Rekombinationstechniken durchgeführt werden.

Die erfindungsgemäßen Nucleinsäuren, Vektoren und regulatorischen oder genetisch mobilen Regionen können außerdem zum Auffinden von Genen verwendet werden, die für Polypeptide codieren, welche funktionell ähnliche Polyketidsynthasen oder funktionell ähnliche Produkte, die an einer Zuckerbiosynthese beteiligt sind, codieren.

Da die erfindungsgemäßen Nucleinsäuren einen umfangreichen Teil des Genoms von S. spinosa ausmacht, können die erfindungsgemäßen Nucleinsäuren als Marker bei der Sequenzierung des Genoms von S. spinosa eingesetzt werden, wodurch die Anordnung von Teilsequenzen eines Genomsequenzierungsprojektes erheblich erleichtert wird.

Somit liefern die erfindungsgemäßen Nucleinsäuren Daten, die im Rahmen eines Genomsequenzierungsprojektes und eines sich darauf aufbauenden Metabolic Engineering zur Steigerung der Spinosynproduktion eingesetzt werden können.

- 23 -

Erläuterungen zu den Abbildungen:

Abbildung 1: Modell für die Biosynthese der Spinosyn-Zucker D-Forosamin und 2, 3, 4-Tri-O-Methyl-L-Rhamnose.

Abbildung 2: Lage, der an der Spinosyn-Biosynthese direkt oder indirekt beteiligten DNA-Regionen 1 (SEQ ID NO: 4) und DNA-Region 2 (SEQ ID NOS: 5 und 6). Die schwarzen Balken im unteren Teil der Abbildung geben schematisch die Positonen der Cosmid-DNA Inserts zueinander und in Bezug zu den DNA-Regionen 1 und 2 an. Die dargestellen Cosmid-Inserts wurden zur Sequenzierung der SEQ ID NOS: 1 bis 3 herangezogen.

Abbildung 3: Schematische Darstellung der Lage der Insert-DNA (schwarze Balken im unteren Teil der Abbildung) der benannten Cosmide, die zur Ankopplung eines Forosamin-Restes oder eines Trimethyl-Rhamnose-Restes durch Biotransformation des Spinosyn-Aglycons und Spinosyn-Pseudoaglycons herangezogen worden sind.

Abbildung 4: Schematische Darstellung der offenen Leserahmen (ORF's) der DNA-Region 3, die der SEQ ID NO: 51 entspricht, auf Cosmid 16-2-2.

Abbildung 5: Schematische Darstellung offener Leserahmen (ORF's) der DNA-Regionen 1 und 2. Die ORF's sind nummeriert von 1 bis 22 entsprechend SEQ ID NOS: 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47 und 49.

Abbildung 6: Schematische Darstellung offener Leserahmen (ORF's) der DNA-Region 2 (SEQ ID NOS: 5 und 6) und ableitbarer Module und Domänen. SM, Startmodul; M1 bis M10, Modul 1 bis Modul 10; KS, β-Ketoacyl:Acyl Carrier Protein Synthase; AT, Acyltransferase; ACP, β-Ketoacyl:Acyl Carrier Protein; KR, Ketoreduktase; DH, Dehydratase; ER, Enoylreduktase; TE, Thioesterase.

Abbildung 7: Schematische Darstellung der Lage von BAC-Shuttleklon Insert-DNA als schwarze Balken im unteren Teil der Abbildung. Die Größe der Insert-DNA beträgt mindestens 100 kb. Durchgezogene Balken: DNA-Sequenz ist identisch mit Teilen der DNA-Region 1 und der Gesamtheit der DNA-Region 2 (P11/G6 und P11/B10) bzw. mit der Gesamtheit der DNA-Region 1 und Teilen der DNA-Region 2 (P8/G11). Gestrichelte Balken: DNA-Sequenz liegt außerhalb des sequenzierten Bereichs.

- 25 -

Beispiele

Bakterienstämme und Plasmide

Escherichia coli XL1-Blue MRF′ und die Cosmidvektoren SuperCos1 (Stratagene, Europe) und pOJ446 (Biermann et àl., 1992) wurden verwendet zur Erstellung von Genbanken von *S. spinosa* ATCC49460 (American Type Culture Collection, U.S.A., EP-A 0 375 316). *E. coli* JM110 (Stratagene, Europe) wurde verwendet zur Propagierung von Plasmiden, die durch Transformation nach *Streptomyces* übertragen wurden. *Streptomyces albus* J1074 (Chater and Wilde, 1980; John Innes Institut in Norwich, UK) wurde zur heterologen Expression von und zur Biotransformation mit Spinosyn-Biosynthesegenen eingesetzt.

Plasmid pBeloBAC11 (Kim et al., 1996) und pOJ446 (Biermann et al., 1992) wurden verwendet zur Herstellung eines *E. coli – Streptomyces* BAC-Shuttlevektors.

Molekularbiologische Methoden

Molekularbiologische Methoden wie DNA-Restriktion, Agarose-Gelelektrophorese von DNA, Ligation von Restriktionsfragmenten, Kultivierung und Transformation von *E. coli* wurden durchgeführt wie beschrieben in Sambrook et. al (1989). Plasmide wurden mit Qiagen Plasmid Kit (Qiagen, Hilden, Deutschland) isoliert. Die verwendeten Enzyme stammten von Roche Diagnostics GmbH (Mannheim, Deutschland).

Anzucht Bedingungen and molekulargenetische Methoden mit *S. spinosa* und Streptomyceten sind beschrieben in (Hopwood et al., 1985). Alle Anzuchten in Flüssigkultur von *S. spinosa* oder Streptomyceten erfolgten aerob in Erlenmeyerkolben bei 28°C.

- 26 -

Die DNA-DNA-Hybridisierungen erfolgten unter Verwendung des DIG-High Prime DNA Labeling and Detection Kit nach Angaben des Herstellers (Roche Diagnostics GmbH, Mannheim, Deutschland).

5   Wachstumsmedien:

LB   Sambrook et. al., 1989

TS   Difco Bestell-Nummer 0 370-17-3 (Difco Detroit, MI, USA)

10

R5A   Illing et al., 1985

Herstellung einer Cosmid Genbank von *S. spinosa*

15   Um eine Genbank von *S. spinosa* zu erhalten, wurde chromosomale DNA von *S. spinosa* ATCC49460 mit *Mbo*I partiell geschnitten und durch Zentrifugation im Glucosedichtegradienten aufgetrennt. Die Cosmid-DNA (SuperCos1, Stratagene Europe) wurde nach Angaben des Herstellers vorbereitet, mit den *S. spinosa* DNA-Fragmenten zwischen 35 und 45 kb ligiert und mit Hilfe des Gigapack-Verpackungs-

20   system (Stratagene Europe) in Phagenpartikel verpackt. Die Transfektion erfolgte in *E. coli* XL-1 blue MRF'. Diese Methode wurde ebenfalls dazu verwendet eine zweite *S. spinosa* Genbank anzulegen unter Verwendung des *E. coli-Streptomyces* Shuttle-Cosmids pOJ446.

25   Sequenzierung des Spinosynbiosynthese-Genclusters und eines DNA-Fragmentes das außerhalb dieses Clusters liegt, dessen Produkte aber an der Biosynthese von Spinosyn beteiligt sind

Die Insert-DNA der SuperCos1 Cosmide 16-1-8, 16-59-1, und 16-59-8 wurden

30   sequenziert. Eine ca. 4 kb große Lücke zwischen den Cosmiden 16-59-1 und 16-1-8

- 27 -

wurde durch pimer walking Sequenzierung eines entsprechenden Teilbereiches von Cosmid 16-59-6 geschlossen.

Eine ca. 2,3 kb große DNA-Sequenz auf dem SuperCos1 Cosmid 16-2-2 wurde

5   sequenziert.

Identifizierung und Charakterisierung von chromosomalen DNA-Fragmenten einer BAC-Shuttlevektor-Genbank aus *S. spinosa*, die Spinosyn-Biosynthesegensequenzen tragen

10

Zur Herstellung des BAC-Shuttlevektors, der nicht nur in *E. coli* sondern auch in Actinomyceten wie *Streptomyces* übertragen und vermehrt werden kann, wurde der Vektor pBeloBAC11 mit *Xho*I linearisiert, und durch die Anwendung von Klenow Polymerase wurden glatte DNA-Enden hergestellt. Ein ca. 6 kb großes *Dra*I –

15   *Eco*RV DNA-Fragment des Cosmidvektors pOJ446, das den Replikationsursprung des Plasmides SCP2*, das Apramycinresistenzgen sowie den *oriT* zum konjugativen Transfer trägt, wurde mit dem linearisierten BAC-Vektor ligiert. Der resultierende Vektor erhielt die Bezeichnung pEBZ333.

20   Ausgehend von partiell mit *Mbo*I geschnittener genomischer DNA des Stammes *S. spinosa* ATCC49460 und dem mit *Bam*HI geschnittenen Vektor pEBZ333 wurde eine BAC-Genbank erstellt.

Analyse und Annotation offener Leserahmen direkt oder indirekt an der Spinosyn-

25   Biosynthese beteiligter DNA-Sequenzen

Ausgehend von der Sequenz gemäß SEQ ID NOS: 1 bis 3 wurden offene Lese-rahmen (ORF's) identifiziert, die direkt oder indirekt an der Biosynthese von Spinosyn beteiligt sind. Diese ORF's wurden in zwei DNA-Regionen unterteilt, die

30   als DNA-Region 1 und DNA-Region 2 (Abb. 2 und 5) bezeichnet werden und die Sequenzen gemäß SEQ ID NO: 4 bzw. 5 und 6 tragen. Die DNA-Region 1 trägt

- 28 -

offene Leserahmen, deren Produkte an der Modifizierung und Tricyclusbildung des Spinosyn-Aglycons beteiligt sind, während die DNA-Region 2 (Abb. 2, 5 und 6) offene Leserahmen umfasst, deren Produkte die Spinosyn-Polyketidsynthase codieren. Die beiden jeweils ersten Nucleotide dieser DNA-Regionen liegen un-

5   mittelbar nebeneinander (Abb. 2, 3 und 5).

Eine weitere DNA-Region 3 (SEQ ID NO: 51) liegt außerhalb dieses Clusters von DNA-Sequenzen und trägt offene Leserahmen, deren Produkte ebenfalls an der Biosynthese des Spinosyn-Zuckers Trimethyl-Rhamnose beteiligt sind.

10

Herstellung des Spinosyn-Aglycons und 17-Pseudoaglycons aus Tracer[®]

Ausgehend von 18,7 g des kommerziell erhältlichen Produktes Tracer[®] wurden nach Gefriertrocknung und Säulenchromatographie an Kieselgel 8,92 g Spinosyn A und D

15   in einem Verhältnis von 82:18 gewonnen.

Die Hydrolyse des Aminozuckers Forosamin gelang mit 2.7 N Schwefelsäure in Ethanol unter Rückfluß. Dabei fiel der Großteil des entstehenden 17-Pseudoaglycons von Spinosyn A/D aus. Im Filtrat wurden neben weiterem 17-Pseudoaglycon in Ab-

20   hängigkeit von der Reaktionsdauer geringe bis mittlere Mengen des Spinosyn-Aglycons gefunden.

Eine vollständige Hydrolyse zum Aglycon gelang unter etwas drastischeren Bedingungen (7.2 N Schwefelsäure in Methanol unter Rückfluß). Die Aglycon-Fraktion

25   enthielt ausschließlich Aglycon von Spinosyn A. Dies stimmt sehr gut mit der Literatur überein (Creemer et al., 1998), die unter entsprechenden Reaktionsbedingungen eine vollständige Zersetzung des Pseudoaglycons von Spinosyn D beschreibt. Als Ursache nehmen die Autoren eine leichtere Protonierung der 5,6-Doppelbindung bei Spinosyn D unter Bildung eines tertiären Carbokations und an-

30   schließende Umlagerungen an.

- 29 -

Es konnten somit ausgehend von 18,7 g käuflichem Tracer® 3,0 g Aglycon von Spinosyn A hergestellt werden.

Tracer (Dow AgroScience)
18.7 g

Gefriertrocknung

grauer Feststoff
10.0 g

Chromatographie

Spinosyn A/D (A, R = H, 82 %; D, R = CH₃, 18 %)

8.92 g

2.7 N H₂SO₄ / EtOH
3 h Rückfluß

69 %   **16 %**

       +

17-Pseudoaglycon von Spinosyn A/D   **Aglycon von Spinosyn A**

(A, R = H, 82 %; D, R = CH₃, 18 %)

64 %

7.2 N H₂SO₄ / MeOH
3 h Rückfluß

- 30 -
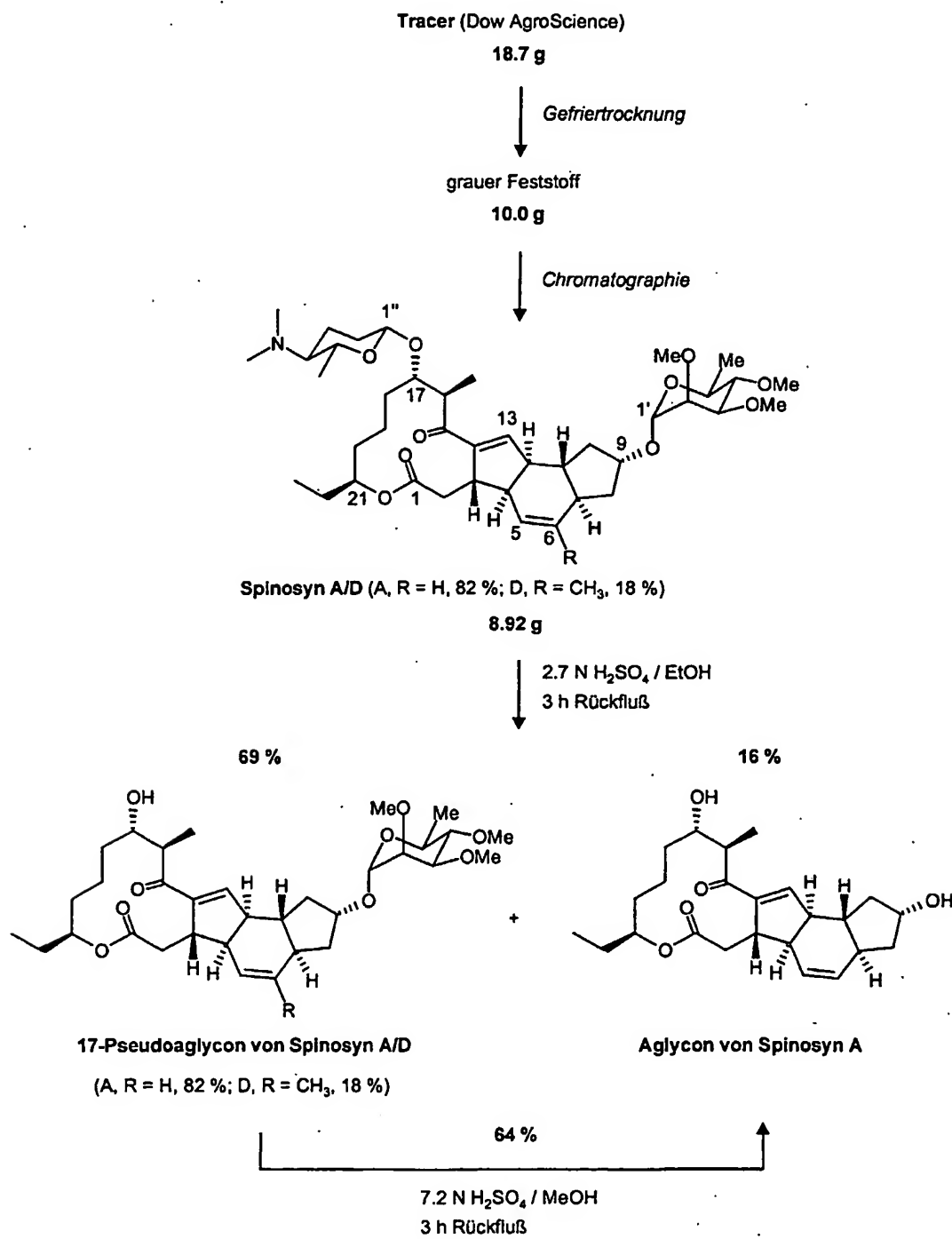
Gewinnung von Spinosyn A/D aus Tracer®

Die Gefriertrocknung von 18,7 g Tracer® lieferten 10,0 g grauen Feststoff. Nach
Säulenchromatographie dieses Feststoffes an 800 cm³ Kieselgel (Eluent: Dichlor-
5   methan/Methanol 95:5) erhielt man 8,92 g reines Spinosyn A/D (82 % A, 18 % D).
– DC: R_f (SiO$_2$, Dichlormethan/Methanol 9:1) = 0,46. – ^{1}H-NMR: CDCl$_3$, δ = 6,77
(s, 13-H); 5,88 (d, 5-H von Spinosyn A); 5,80 (m, 6-H von Spinosyn A); 5,49 (m,
5-H von Spinosyn D); 4,87 (d, 1'-H); 4,67 (m, 21-H); 4,43 (d, 1''-H); 4,31 (m, 9-H)
u. a. – LC/MS: Elektrospray Positiv; Peak bei RT 44,0 min: m/z = 733 (100 %)
10   [M+H]$^+$ (Spinosyn A); Peak bei 44,7 min: m/z = 747 (100 %) [M+H]$^+$ (Spinosyn D).

Darstellung des 17-Pseudoaglycons von Spinosyn A/D:

8,65 g (11,81 mmol) Spinosyn A/D wurden in 61 ml Ethanol gelöst und mit 104 ml
15   Wasser und 208 ml 4 N H$_2$SO$_4$ versetzt. Nach 3 h Erwärmen unter Rückfluß wurde
der ausgefallene Feststoff (A) abfiltriert und getrennt vom Filtrat (B) aufgearbeitet.
Der Feststoff (A) wurde mit 1 N H$_2$SO$_4$ gewaschen, in 140 ml Dichlormethan aufge-
nommen, nacheinander mit gesätt. NaHCO$_3$-Lösung und gesätt. NaCl-Lösung ge-
waschen, über Na$_2$SO$_4$ getrocknet und im Vakuum eingeengt. Umkristallisation aus
20   Ethanol lieferten 3,03 g 17-Pseudoaglycon von Spinosyn A/D und Mutterlauge (C).
Das Filtrat (B) wurde mehrmals mit Dichlormethan extrahiert. Die Extrakte wurden
nacheinander mit gesätt. NaHCO$_3$-Lösung und gesätt. NaCl-Lösung gewaschen, über
Na$_2$SO$_4$ getrocknet und im Vakuum eingeengt. Der Rückstand wurde vereint mit der
im Vakuum eingeengten Mutterlauge (C) und durch Säulenchromatographie an
25   650 cm³ Kieselgel (Eluent: Cyclohexan/Essigsäureethylester 1:1, dann 100 % Essig-
säureethylester) aufgetrennt. Man erhielt neben weiteren 1,76 g 17-Pseudoaglycon
von Spinosyn A/D 0,78 g (16 %) Aglycon von Spinosyn A. Die Gesamtausbeute von
17-Pseudoaglycon von Spinosyn A/D betrug 4,79 g (69 %). – a) 17-Pseudoaglycon
von Spinosyn A/D (82 % A, 18 % D): DC: R_f (SiO$_2$, Essigsäureethylester) = 0,48.
30   –^{1}H-NMR: CDCl$_3$, δ = 6,78 (s, 13-H); 5,88 (d, 5-H von Spinosyn A); 5,80 (m, 6-H
von Spinosyn A); 5,49 (m, 5-H von Spinosyn D); 4,86 (d, 1'-H); 4,70 (m, 21-H);

4,32 (m, 9-H) u. a. - LC/MS: Elektrospray Positiv; Peak bei RT 40,7 min: m/z = 609 (100 %) $[M+NH_4]^+$, m/z = 641 (10 %) $[M+NH_4+CH_3OH]^+$ (Pseudoaglycon von Spinosyn A); Peak bei RT 41,4 min: m/z = 623 (100 %) $[M+NH_4]^+$, m/z = 655 (8 %) $[M+NH_4+CH_3OH]^+$ (Pseudoaglycon von Spinosyn D). – b) Aglycon von Spinosyn A: DC: R_f (SiO$_2$, Essigsäureethylester) = 0,29. – ^{1}H-NMR: CDCl$_3$, δ = 6,80 (s, 13-H); 5,89 (d, 5-H); 5,80 (m, 6-H); 4,70 (m, 21-H); 4,44 (m, 9-H) u. a. - LC/MS: Elektrospray Positiv; Peak bei RT 36,8 min: m/z = 420 (100 %) $[M+NH_4]^+$, m/z = 452 (10 %) $[M+NH_4+CH_3OH]^+$.

Darstellung des Aglycon von Spinosyn A/D

4,30 g (7,29 mmol) Pseudoaglycon von Spinosyn A/D wurden in 190 ml Methanol gelöst und mit 285 ml 7,2 N H$_2$SO$_4$ versetzt. Nach 3 h Erwärmen unter Rückfluß wurde die abgekühlte Reaktionsmischung vorsichtig in 1700 ml gesättigte NaHCO$_3$-Lösung gegeben. Man extrahierte mit Diethylether, wusch die Extrakte nacheinander mit gesätt. NaHCO$_3$-Lösung und gesätt. NaCl-Lösung, trocknete über Na$_2$SO$_4$ und engte im Vakuum ein. Nach Säulenchromatographie dieses Feststoffes an 650 cm^3 Kieselgel (Eluent: Cyclohexan/Essigsäureethylester 1:2, dann 100 % Essigsäureethylester) erhielt man 1,88 g (64 %) Aglycon von Spinosyn A. – DC: R_f (SiO$_2$, Essigsäureethylester) = 0,29. – ^{1}H-NMR: CDCl$_3$, δ = 6,80 (s, 13-H); 5,89 (d, 5-H); 5,80 (m, 6-H); 4,70 (m, 21-H); 4,44 (m, 9-H) u. a. – LC/MS: Elektrospray Positiv; Peak bei RT 36,6 min: m/z = 420 (100 %) $[M+NH_4]^+$, m/z = 452 (14 %) $[M+NH_4+CH_3OH]^+$ (Aglycon von Spinosyn A).

Forosaminylierung des Spinosyn-Aglycons und Anknüpfung eines Trimethyl-Rhamnosezuckers an das Spinosyn-Aglycon durch Biotransformation mit einem rekombinanten *Streptomyces* Stamm, der Spinosyn-Zuckerbiosynthesegene heterolog exprimiert

20 ml R5A Medium (Illing et al., 1989) mit 5 μg Apramycin / ml wurde mit Mycel des rekombinanten Stammes *S. albus* (165-1) oder *S. albus* (165-8) angeimpft und

24 h aerob bei 28°C bebrütet. Diese Kultur wurde mit 50 µg/ml des hergestellten Spinosyn-Aglycons (100 µl einer 1 %igen Stammlösung in Methanol; Herstellung siehe Kapitel "Herstellung des Spinosyn-Aglycons und 17-Pseudoaglycons aus Tracer®", „Gewinnung von Spinosyn A/D aus Tracer®" und „Darstellung des Aglycon von Spinosyn A/D") versetzt und ca. 120 h bei 28°C aerob inkubiert. Als Kontrolle wurde in gleicher Weise *S. albus* (pEBZ340; pOJ446-Vektor mit einem ca. 1,8 kb großen Spinosyn-PKS tragenden DNA-Fragment aus Cosmid 16-1-8) kultiviert und mit Spinosyn-Aglycon versetzt. Die Kulturen wurden nach Inkubation zur Abtrennung von Zellmycel zentrifugiert und der Überstand (20 ml) wurde mit 25 ml Methanol versetzt.

Je 35 ml des mit Methanol versetzten Kulturüberstandes wurden lyophylisiert, mit 15 ml Wasser aufgenommen und zweimal mit je 10 ml Essigsäureethylester extrahiert. Die vereinten organischen Phasen wurden zur Trockene eingeengt und mit 350 µl Methanol aufgenommen. Ein Aliquot dieser Extrakte wurde mittels LC/MS mit Elektrospray Positiv-Ionisation untersucht.

Der Kulturüberstand der Anzucht von *S. albus* (165-1) enthielt eine Verbindung mit dem Molekulargewicht eines forosaminylierten Aglycons von Spinosyn A sowie Spinosyn A.

Peak 1: RT = 41,0 min: m/z = 544 (100 %) $[M+H]^+$, m/z = 576 (16 %) $[M+H+CH_3OH]^+$ (Forosaminyliertes Aglycon von Spinosyn A); LC/MS/MS: m/z = 142 (38 %) (Forosamin-Fragment).
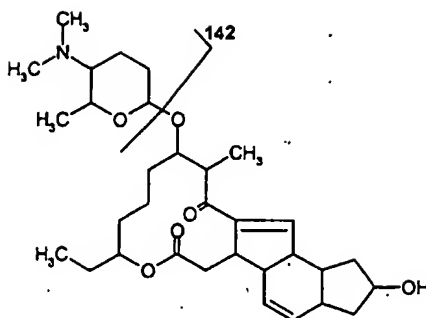
Forosaminyliertes Aglycon von Spinosyn A
Molekulargewicht = 543
Summenformel = $C_{32}H_{49}NO_6$

Peak 2: RT = 44,2 min: m/z = 733 (100 %) $[M+H]^+$ (Spinosyn A); LC/MS/MS: m/z = 142 (21 %) (Forosamin-Fragment).

Der Kulturüberstand von *S. albus* (165-8) enthielt eine Verbindung mit dem Molekulargewicht eines Forosaminylierten Aglycons von Spinosyn A.

Peak 1: RT = 40,9 min: m/z = 544 (100 %) $[M+H]^+$, m/z = 576 (16 %) $[M+H+CH_3OH]^+$ (Forosaminyliertes Aglycon von Spinosyn A); LC/MS/MS: m/z = 142 (39 %) (Forosamin-Fragment).

Der Kulturüberstand von *S .albus* (pEBZ340) enthielt keine Verbindungen mit MW 543 und kein Spinosyn A.

Forosaminylierung des Spinosyn-17-Pseudoaglycons durch Biotransformation mit einem rekombinanten *Streptomyces* Stamm, der Spinosyn Zuckerbiosynthesegene heterolog exprimiert

20 ml R5A Medium (Illing et al., 1989) mit 5 µg Apramycin / ml wurde mit Mycel des rekombinanten Stammes *S. albus* (165-1) oder *S. albus* (165-8) angeimpft und 24 h aerob bei 28°C bebrütet. Diese Kultur wurde mit 50 µg/ml des hergestellten 17-Pseudoaglycons von Spinosyn (100 µl einer 1 %igen Stammlösung in Methanol; Herstellung siehe Kapitel "Herstellung des Spinosyn-Aglycons und 17-Pseudoaglycons aus Tracer®", „Gewinnung von Spinosyn A/D aus Tracer®" und „Dar-

- 34 -

stellung des 17-Pseudoaglycon von Spinosyn A/D") versetzt und ca. 120 h bei 28°C aerob inkubiert. Die Kulturen wurden nach Inkubation zur Abtrennung von Zellmycel zentrifugiert und der Überstand (20 ml) wurde mit 25 ml Methanol versetzt.

5

Je 35 ml des mit Methanol versetzten Kulturüberstandes wurden lyophylisiert, mit 15 ml Wasser aufgenommen und zweimal mit je 10 ml Essigsäureethylester extrahiert. Die vereinten organischen Phasen wurden zur Trockene eingeengt und mit 350 µl Methanol aufgenommen. Ein Aliquot dieser Extrakte wurde mittels LC/MS

10   mit Elektrospray Positiv-Ionisation untersucht.

Der Kulturüberstand von *S. albus* (165-1) enthielt Spuren von Spinosyn A und D.
Peak 1: RT = 44,2 min: m/z = 733 (100 %) $[M+H]^+$ (Spinosyn A); LC/MS/MS: m/z = 142 (8 %) (Forosamin-Fragment).

15   Peak 2: RT = 44,7 min: m/z = 747 (100 %) $[M+H]^+$ (Spinosyn D); LC/MS/MS: m/z = 142 (37 %) (Forosamin-Fragment).

Der Kulturüberstand von *S. albus* (165-8) enthielt Spuren von Spinosyn A und D.
Peak 1: RT = 44,1 min: m/z = 733 (100 %) $[M+H]^+$ (Spinosyn A).

20   Peak 2: RT = 44,7 min: m/z z = 747 (100 %) $[M+H]^+$ (Spinosyn D).

Hinterlegung von Mikroorganismen

Folgende Mikroorganismen und Plasmide sind bei der Deutschen Sammlung von

25   Mikroorganismen und Zellkulturen GmbH (DSMZ), Mascheroder Weg 1b, D- 38124 Braunschweig, in Übereinstimmung mit den Bestimmungen des Budapester Vertrages hinterlegt worden.

Mikroorganismus und Plasmid	Hinterlegungs-nummer	Datum
E. coli XL1-Blue MRF'mit Cosmid 16-1-8	DSM 12961	1999-08-02
E. coli XL1-Blue MRF'mit Cosmid 16-2-2	DSM 12962	1999-08-02
E. coli XL1-Blue MRF'mit Cosmid 16-59-1	DSM 12963	1999-08-02
E. coli XL1-Blue MRF'mit Cosmid 16-59-6	DSM 12964	1999-08-02
E. coli XL1-Blue MRF'mit Cosmid 16-59-8	DSM 12965	1999-08-02
E. coli XL1-Blue MRF'mit Cosmid 165-1	DSM 13005	1999-08-18
E. coli XL1-Blue MRF'mit Cosmid 165-8	DSM 13007	1999-08-18
E. coli DH10B mit dem BAC Shuttle-Klon P8 / G11	DSM 13012	1999-08-18
E. coli DH10B mit dem BAC Shuttle-Klon P11 / B10	DSM 13011	1999-08-18
E. coli DH10B mit dem BAC Shuttle-Klon P11 / G6	DSM 13010	1999-08-18

Literatur

Biermann M., Logan R., O'Brien K., Seno E.T., Nagaraja R., Schoner B.E. (1992) Plasmid cloning vectors for the conjugal transfer of DNA from *Escherichia coli* to *Streptomyces* spp. Gene 116: 43-49

Chater K., Wilde L. (1980) *Streptomyces albus* G Mutants defective in the *Sal*GI restriction-modification system. J. Gen. Microbiol. 116: 323-334.

Devereux J., Haeberli P., Smithies (1984) A comprehensive set of sequence analysis programs for the VAX. Nucleic Acids Research 12: 387-395.

Mertz F., Yao R.C. (1990) *Saccharopolyspora spinosa* sp. nov. isolated from soil collected in a sugar mill rum still. Int. J. Syst. Bacteriol. 40: 34-39.

Creemer L.C., Kirst H.A., Paschal J.W. (1998) Conversion of spinosyn A and spinosyn D to their respective 9- and 17-pseudoaglycones and their aglycones. J. Antibiotics 51: 795-800.

- 36 -

Fishman S.E., Hershberger C.L. (1983) Amplified DNA in *Streptomyces fradiae*. J. Bacteriol. 155: 459-466.

Hopwood D.A., Bibb M.J., Chater K.F., Kieser T., Bruton C.J., Kieser H.M., Lydiate D.J., Smith C.P., Ward J.M., Schrempf H. (1985) Gentic manipulation of *streptomyces* a laboratory manual, The John Innes Foundation, Norwich, 1985.

Illing G.T.; Normansell I.D., Peberdy J.F. (1989) Protoplast isolation and regeneration *in Streptomyces clavuligerus*. J. Gen. Microbiol. 135: 2289-2297.

Kim U.J. Birren B.W. Slepak T. Mancino: V. Boysen C. Kang H.L. Simon M.I. Shizuya H. (1996), Construction and characterization of a human bacterial artificial chromosome library. Genomics 34: 213-218.

Kirst H.A., Michel K.H., Martin J.W., Creemer L.C., Chao E.H., Yao R.C., Nakatsukasa W.M., Boeck L.D., Occolowitzh J.L., Paschal J.W., Deeter J.B., Jones N.D., Thompson G.D. (1991) Tetrahedron Lett. 32: 4839-4842.

Motamedi H., Shafiee A., Sheng-Jian C. (1995) Integrative vectors for heterologous gene expression in *Streptomyces* spp. Gene 160: 25-31.

Muyrers J.P.P., Zhang Y., Testa G., Stewart A.F. (1999) Rapid modification of bacterial artificial chromosomes by ET-recombination. Nucleic Acids Research 27: 1555-1557.

Nakatsukasa W.M., Mabe J.A., Michel K.H., Martin J.W., Paschal J.W., Elzey T.K. (1990) Abstracts of 2nd Int. Conf. on Biotechnology of Microbial Prod.: P-21.

Sambrook J., Fritsch E.F., Maniatis T. (1989) Molecular cloning – A laboratory manual. Second edition. Cold Spring Harbor Laboratory Press.

Shizuya H., Birren B., Kim U.-J., Mancino V., Slepak T., Tachiiri Y., Simon M.I. (1992) Cloning and stable maintenance of 300-kilobase-pair fragments of human DNA in *Escherichia coli* using an F-factor-based vector. Proc. Natl. Acad. Sci. USA 89: 8794-8797.

Smokvina T., Mazodier P., Boccard F., Thompson C.J., Guérineau M. (1990) Construction of a series of pSAM2-based integrative vectors for use in actinomycetes. Gene 94: 53-59.

Patentansprüche

1.   Nucleinsäure, welche zumindest eine Region umfasst, die für eine Enzym-
     aktivität codiert, welche an der Biosynthese von Spinosynen beteiligt ist.

2.   Nucleinsäure gemäß Anspruch 1, dadurch gekennzeichnet, dass es sich um
     einzelsträngige oder doppelsträngige DNA oder RNA handelt.

3.   Nucleinsäure gemäß Anspruch 2, dadurch gekennzeichnet, dass es sich um
     ein DNA-Fragment handelt.

4.   Nucleinsäure gemäß Anspruch 3, dadurch gekennzeichnet, dass sie alle
     Regionen umfasst, die für Enzymaktivitäten codieren, welche an der Bio-
     synthese von Spinosynen beteiligt sind.

5.   Nucleinsäure gemäß einem der Ansprüche 1 bis 4, dadurch gekennzeichnet,
     dass es sich um Enzymaktivitäten von Polyketidsynthasen, Methyltrans-
     ferasen, Glycosyltransferasen, Epimerasen, Aminotransferasen, Dimethyl-
     transferasen, Reduktasen, Dehydratasen und/oder Cyclisierungsenzymen
     handelt.

6.   Nucleinsäure gemäß einem der Ansprüche 1 bis 5, dadurch gekennzeichnet,
     dass sie aus *Saccharopolyspora spinosa* stammt.

7.   Nucleinsäure gemäß Anspruch 1, umfassend zumindest eine Sequenz ausge-
     wählt aus

     (a)   den Sequenzen gemäß SEQ ID NOS: 1, 2, 3, 4, 5, 6, 7, 9, 11, 13, 15,
           17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 52
           oder 54,

(b)   zumindest 14 Basenpaare langen Teilsequenzen der unter (a) definierten Sequenzen,

(c)   Sequenzen, welche an die unter (a) definierten Sequenzen hybridisieren

(d)   Sequenzen, welche eine zumindest 70 %ige Identität zu den unter (a) definierten Sequenzen aufweisen,

(e)   Sequenzen, welche zu den unter (a) definierten Sequenzen komplementär sind, und

(g)   Sequenzen, welche aufgrund der Degeneriertheit des genetischen Codes für dieselbe Aminosäuresequenz kodieren wie die unter (a) bis (d) definierten Sequenzen.

8.   Nucleinsäure gemäß Anspruch 7, dadurch gekennzeichnet, dass sie die Sequenz gemäß SEQ ID NOS: 1 bis 6 umfasst.

9.   Nucleinsäure gemäß Anspruch 7, dadurch gekennzeichnet, dass sie die Sequenz gemäß SEQ ID NO: 4 umfasst.

10.   Nucleinsäure gemäß Anspruch 7, dadurch gekennzeichnet, dass sie die Sequenz gemäß SEQ ID NOS: 5 und 6 umfasst.

11.   Nucleinsäure gemäß Anspruch 7, dadurch gekennzeichnet, dass sie zumindest eine Sequenz gemäß SEQ ID NOS: 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37 oder 39 umfasst.

12.   Nucleinsäure gemäß Anspruch 7, dadurch gekennzeichnet, dass sie zumindest eine Sequenz gemäß SEQ ID NOS: 41, 43, 45, 47 oder 49 umfasst.

13.   Regulatorische Region, welche die Transkription einer Nukleinsäure gemäß
        einem der Ansprüche 1 bis 7 in *Saccharopolyspora spinosa* kontrolliert.

14.   DNA-Konstrukt umfassend eine Nucleinsäure gemäß einem der Ansprüche 1
        bis 12 und zumindest einen heterologen Promotor.

15.   Vektor umfassend zumindest eine Nucleinsäure gemäß einem der Ansprüche
        1 bis 12, eine regulatorische Region gemäß Anspruch 13 oder ein DNA-
        Konstrukt gemäß Anspruch 14.

16.   Vektor gemäß Anspruch 15, dadurch gekennzeichnet, dass die Nucleinsäure
        funktionell mit regulatorischen Sequenzen verknüpft ist, welche die Ex-
        pression der codierenden Regionen der Nucleinsäure in pro- oder eukaryo-
        tischen Zellen gewährleisten.

17.   Vektor gemäß Anspruch 15 oder 16, dadurch gekennzeichnet, dass es sich um
        einen BAC-Vektor, PAC-Vektor oder einen zu BAC- oder PAC-Vektoren
        funktionell gleichwertigen Vektor handelt.

18.   Vektor gemäß Anspruch 17, dadurch gekennzeichnet, dass es sich um einen
        Vektor handelt, der den BAC-Klonen mit den Hinterlegungsnummern DSM
        13010, DSM 13011 oder DSM 13012 entspricht.

19.   Vektor gemäß einem der Ansprüche 15 bis 18, dadurch gekennzeichnet, dass
        es sich um einen Shuttle-Vektor handelt, der sowohl in Prokaryonten als auch
        in Eukaryonten übertragbar ist.

20.   Vektor gemäß einem der Ansprüche 15 bis 19, dadurch gekennzeichnet, dass
        es sich um einen Shuttle-Vektor handelt, der sowohl in Gram-negative und in
        Gram-positive Bakterien als auch in Archea übertragbar ist.

21. Vektor gemäß einem der Ansprüche 15 bis 19, dadurch gekennzeichnet, dass es sich um einen Shuttle-Vektor handelt, der sowohl in *Escherichia coli* als auch in Actinomyceten übertragbar ist.

22. Vektor gemäß Anspruch 21, dadurch gekennzeichnet, dass es sich um einen Shuttle-Vektor handelt, der sowohl in *Escherichia coli* als auch in *Streptomyces* übertragbar ist.

23. Vektor gemäß einem der Ansprüche 15 bis 22, dadurch gekennzeichnet, dass er in einem Prokaryonten autonom replizierbar ist.

24. Vektor gemäß einem der Ansprüche 15 bis 22, dadurch gekennzeichnet, dass er in einem Prokaryonten unter Beteiligung des Phagen ΦC31-, des pSAM2- oder des Mini-Circle-Integrationsmechanismus ins Genom integrierbar ist.

25. Vektor gemäß einem der Ansprüche 15 bis 22, dadurch gekennzeichnet, dass er in einem Prokaryonten durch RecA-vermittelte Rekombination ins Genom integrierbar ist.

26. Vektor gemäß einem der Ansprüche 15 bis 22, dadurch gekennzeichnet, dass er in einem Prokaryonten durch RecE- und RecT-vermittelte Rekombination ins Genom integrierbar ist.

27. Wirtszelle enthaltend eine Nucleinsäure gemäß einem der Ansprüche 1 bis 12, eine regulatorische Region gemäß Anspruch 13, ein DNA-Konstrukt gemäß Anspruch 14 oder zumindest einen Vektor gemäß einem der Ansprüche 15 bis 26.

28. Wirtszelle gemäß Anspruch 27, dadurch gekennzeichnet, dass es sich um eine pro- oder eukaryotische Zelle handelt.

29.   Wirtszelle gemäß Anspruch 28, dadurch gekennzeichnet, dass die prokaryo-
        tische Zelle zur Gruppe der Actinomyceten, bevorzugt zur Gruppe der Strep-
        tomyceten gehört.

30.   Wirtszelle gemäß Anspruch 28, dadurch gekennzeichnet, dass die eukaryo-
        tische Zelle eine Pflanzenzelle ist.

31.   Polypeptid, welches von einer Nucleinsäure gemäß einem der Ansprüche 1
        bis 7 codiert wird.

32.   Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivi-
        tät einer Methyltransferase aufweist.

33.   Polypeptid gemäß Anspruch 32, dadurch gekennzeichnet, dass es die Amino-
        säuresequenz gemäß SEQ ID NOS: 8, 12, 14, 18 oder 20, oder eine Teil-
        sequenz davon aufweist.

34.   Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivi-
        tät einer Glycosyltransferase aufweist.

35.   Polypeptid gemäß Anspruch 34, dadurch gekennzeichnet, dass es die Amino-
        säuresequenz gemäß SEQ ID NOS: 10 oder 30, oder eine Teilsequenz davon
        aufweist.

36.   Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivi-
        tät eines C-C verknüpfenden Enzyms, das Cyclisierungsreaktionen durch-
        führt, aufweist.

37.   Polypeptid gemäß Anspruch 36, dadurch gekennzeichnet, dass es die Amino-
        säuresequenz gemäß SEQ ID NO: 16 oder eine Teilsequenz davon aufweist.

38.   Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität eines Enzyms, das an Cyclisierungsreaktionen beteiligt ist, aufweist.

5   39.   Polypeptid gemäß Anspruch 38, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NO: 22 oder eine Teilsequenz davon aufweist.

40.   Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität einer 2,3-Reduktase aufweist.

10

41.   Polypeptid gemäß Anspruch 40, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NO: 24 oder eine Teilsequenz davon aufweist.

42.   Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität einer 2,3-Dehydratase aufweist.

15

43.   Polypeptid gemäß Anspruch 42, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NO: 26 oder eine Teilsequenz davon aufweist.

20   44.   Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität einer Thioesterase aufweist.

45.   Polypeptid gemäß Anspruch 44, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NO: 28 oder eine Teilsequenz davon aufweist.

25

46.   Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität einer 3,4-Dehydratase aufweist.

47.   Polypeptid gemäß Anspruch 46, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NO: 32 oder eine Teilsequenz davon aufweist.

30

- 44 -

48. Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität einer 4-Aminotransferase aufweist.

49. Polypeptid gemäß Anspruch 48, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NO: 34 oder eine Teilsequenz davon aufweist.

50. Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität einer N-Dimethyltransferase aufweist.

51. Polypeptid gemäß Anspruch 50, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NO: 36 oder eine Teilsequenz davon aufweist.

52. Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität einer 3,4-Reduktase aufweist.

53. Polypeptid gemäß Anspruch 52, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NO: 38 oder eine Teilsequenz davon aufweist.

54. Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität eines Transkriptions-Regulators aufweist.

55. Polypeptid gemäß Anspruch 54, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NO: 40 oder eine Teilsequenz davon aufweist.

56. Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität einer Polyketidsynthase aufweist.

57. Polypeptid gemäß Anspruch 56, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NOS:: 42, 44, 46, 48 oder 50, oder eine Teilsequenz davon aufweist.

58. Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität einer Glucose-Dehydratase aufweist.

59. Polypeptid gemäß Anspruch 58, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NO: 53 aufweist.

60. Polypeptid gemäß Anspruch 31, dadurch gekennzeichnet, dass es die Aktivität einer 3,5-Epimerase aufweist.

61. Polypeptid gemäß Anspruch 60, dadurch gekennzeichnet, dass es die Aminosäuresequenz gemäß SEQ ID NO: 55 aufweist.

62. Enzyme, die an Cyclisierungsreaktionen beteiligt sind, dadurch gekennzeichnet, dass sie die Aminosäuresequenz gemäß SEQ ID NO: 15 oder 22, oder eine Teilsequenz davon, welche zumindest noch eine Teilreaktion durchführen kann, umfassen oder eine mindestens 50 %ige Identität dazu auf Aminosäureebene aufweisen.

63. Antikörper, welcher spezifisch mit einem Polypeptid gemäß einem der Ansprüche 31 bis 62 reagiert.

64. Verfahren zur Herstellung einer Nucleinsäure gemäß einem der Ansprüche 1 bis 7, umfassend die folgenden Schritte:

(a) Vollständige chemische Synthese auf an sich bekannte Weise oder

(b) chemische Synthese von Oligonucleotiden, Markieren der Oligonucleotide, Hybridisieren der Oligonucleotide an DNA einer genomischen oder cDNA-Bank, die ausgehend von genomischer DNA bzw. mRNA aus *S. spinosa* hergestellt wurde, Selektieren von

- 46 -

positiven Klonen und Isolieren der hybridisierenden DNA aus positiven Klonen oder

(c)   chemische Synthese von Oligonucleotiden und Amplifizierung der Ziel-DNA mittels PCR.

65.   Verfahren zur Herstellung eines Polypeptids gemäß einem der Ansprüche 31 bis 62, umfassend die folgenden Schritte:

(a)   Kultivieren einer Wirtszelle gemäß einem der Ansprüche 27 bis 30 unter Bedingungen, die die Expression der Nucleinsäure gemäß einem der Ansprüche 1 bis 7 gewährleisten, oder

(a1)   Exprimieren einer Nucleinsäure gemäß einem der Anprüche 1 bis 7 in einem *in vitro*-System, und

(b)   Gewinnen des Polypeptids aus der Zelle, dem Kulturmedium oder dem *in vitro*-System.

66.   Verfahren zum Herstellen von Spinosyn, Spinosyn-Vorstufen oder Spinosyn-Derivaten umfassend die folgenden Schritte:

(a)   Kultivieren einer Wirtszelle gemäß einem der Ansprüche 27 bis 30 unter Bedingungen, die die Expression der Nucleinsäure gemäß einem der Ansprüche 1 bis 7 gewährleisten und

(b)   Gewinnen des Spinosyns, der Spinosyn-Vorstufe oder des Spinosyn-Derivates aus der Zelle oder dem Kulturmedium.

67.   Verfahren zum Herstellen von Spinosyn-Derivaten, einschließlich Spinosyn-Vorstufen, umfassend die folgenden Schritte:

(a)   Austauschen zumindest einer Modul-codierenden Nucleinsäure-sequenz gemäß Anspruch 7 gegen zumindest eine andere Modul-codierende Nucleinsäuresequenz gemäß Anspruch 7, oder

5

(b)   Austauschen zumindest einer Modul-codierenden Nucleinsäure-sequenz gemäß Anspruch 7 gegen zumindest eine andere Modul-codierende Nucleinsäuresequenz aus *S. spinosa,* oder

10   (c)   Austauschen zumindest einer Modul-codierenden Nucleinsäure-sequenz gemäß Anspruch 7 gegen zumindest eine andere Modul-codierende Nucleinsäuresequenz aus einem anderen Organismus als *S. spinosa,* oder

15   (d)   Austauschen zumindest einer Domänen-codierenden Nucleinsäure-sequenz gemäß Anspruch 7 gegen zumindest eine andere Domänen-codierende Nucleinsäuresequenz gemäß Anspruch 7, oder

(e)   Austauschen zumindest einer Domänen-codierenden Nucleinsäure-
20   sequenz gemäß Anspruch 7 gegen zumindest eine andere Domänen-codierende Nukleinsäuresequenz aus *S. spinosa,* oder

(f)   Austauschen zumindest einer Domänen-codierenden Nucleinsäure-sequenz gemäß Anspruch 7 gegen zumindest eine andere Domänen-
25   codierende Nucleinsäuresequenz aus einem anderen Organismus als *S. spinosa,* oder

(g)   Austauschen einer ersten Acyltransferase-codierenden Nucleinsäure-sequenz gemäß Anspruch 7 gegen eine zweite Acyltransferase-
30   codierende Nucleinsäuresequenz gemäß Anspruch 7, wobei die zweite

- 48 -

Acyltransferase eine unterschiedliche Substratspezifität aufweist als die erste Acyltransferase, oder

(h)   Austauschen einer ersten Acyltransferase-codierenden Nucleinsäuresequenz gemäß Anspruch 7 gegen eine zweite Acyltransferase-codierende Nucleinsäuresequenz aus *S. spinosa*, wobei die zweite Acyltransferase eine unterschiedliche Substratspezifität aufweist als die erste Acyltransferase, oder

(i)   Austauschen einer ersten Acyltransferase-codierenden Nucleinsäuresequenz gemäß Anspruch 7 gegen eine zweite Acyltransferase-codierende Nucleinsäuresequenz aus einem anderen Organismus als *S. spinosa*, wobei die zweite Acyltransferase eine unterschiedliche Substratspezifität aufweist als die erste Acyltransferase, oder

(j)   Deletieren zumindest einer Domänen-codierender Nucleinsäuresequenz gemäß Anspruch 7, oder

(k)   Integratieren zumindest einer Domänen-codierenden Nucleinsäuresequenz gemäß Anspruch 7 in eine Modul-codierende Nucleinsäuresequenz gemäß Anspruch 7, oder

(l)   Mutagenisieren zumindest einer Domänen-codierenden Nucleinsäuresequenz gemäß Anspruch 7,

und Exprimieren der rekombinierten Nucleinsäuresequenz in einer Wirtszelle unter Bedingungen, welche die Synthese eines Spinosyn-Derivates oder einer Spinosyn-Vorstufe erlauben.

68.   Verwendung einer Nucleinsäure gemäß einem der Ansprüche 1 bis 7 zum Identifizieren, Inaktivieren und/oder Modifizieren von Genen der Spinosyn-Biosynthese.

5   69.   Verwendung einer Nucleinsäure gemäß einem der Ansprüche 1 bis 7 zum Erzeugen einer Bibliothek aus Polyketidsynthasen.

70.   Verfahren zum Anfügen eines Forosamin-Zuckerrestes an das Spinosyn-Aglycon oder an das Spinosyn-17-Pseudoaglycon oder an ein Polyketid-
10   Aglycon, umfassend die folgenden Schritte:

    (a)   Übertragen einer Nucleinsäure gemäß SEQ ID NOS: 23, 25, 29, 31, 33, 35 und 37 in eine Wirtszelle, die das Spinosyn-Aglycon oder das Spinosyn-17-Pseudoaglycon oder das Polyketid-Aglycon herstellen
15   kann, oder

    (a1)   Übertragen einer Nucleinsäure gemäß SEQ ID NOS: 23, 25, 29, 31, 33, 35 und 37 in eine Wirtszelle, die das Spinosyn-Aglycon oder das Spinosyn-17-Pseudoaglycon oder das Polyketid-Aglycon nicht her-
20   stellen kann und Zufügen des Spinosyn-Aglycons oder des Spinosyn-17-Pseudoaglycons oder des Polyketid-Aglycons zum Kulturmedium, und

    (b)   Kultivieren der Wirtszelle unter Bedingungen, die zu einem aktiven
25   Stoffwechsel der Zelle führen.

71.   Verfahren zum Anfügen eines Trimethyl-Rhamnose-Zuckerrestes an das Spinosyn-Aglycon oder an das Spinosyn-9-Pseudoaglycon oder an ein Polyketid-Aglycon, umfassend die folgenden Schritte:

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- 50 -

(a)   Übertragen einer Nucleinsäure gemäß SEQ ID NO: 7, 9, 11, 13, 17
        und/oder 19 in eine Wirtszelle, die das Spinosyn-Aglycon oder das
        Spinosyn-9-Pseudoaglycon oder das Polyketid-Aglycon herstellen
        kann, oder

5

(a1)   Übertragen einer Nucleinsäure gemäß SEQ ID NO: 7, 9, 11, 13, 17
        und/oder 19 in eine Wirtszelle, die das Spinosyn-Aglycon oder das
        Spinosyn-9-Pseudoaglycon oder das Polyketid-Aglycon nicht her-
        stellen kann und Zufügen des Spinosyn-Aglycons oder des Spinosyn-
10   9-Pseudoaglycons oder des Polyketid-Aglycons zum Kulturmedium,
        und

(b)   Kultivieren der Wirtszelle unter Bedingungen, die zu einem aktiven
        Stoffwechsel der Zelle führen.

15

72.   Verfahren gemäß Anspruch 71, dadurch gekennzeichnet, dass im Schritt (a)
      Nucleinsäuren gemäß SEQ ID NOS: 9, 11, 13 und 17 übertragen werden.

Fig. 1

Modell für die Biosynthese der Spinosyn Zucker
D-Forosamin und 2,3,4 Tri-O-Methyl-L-Rhamnose
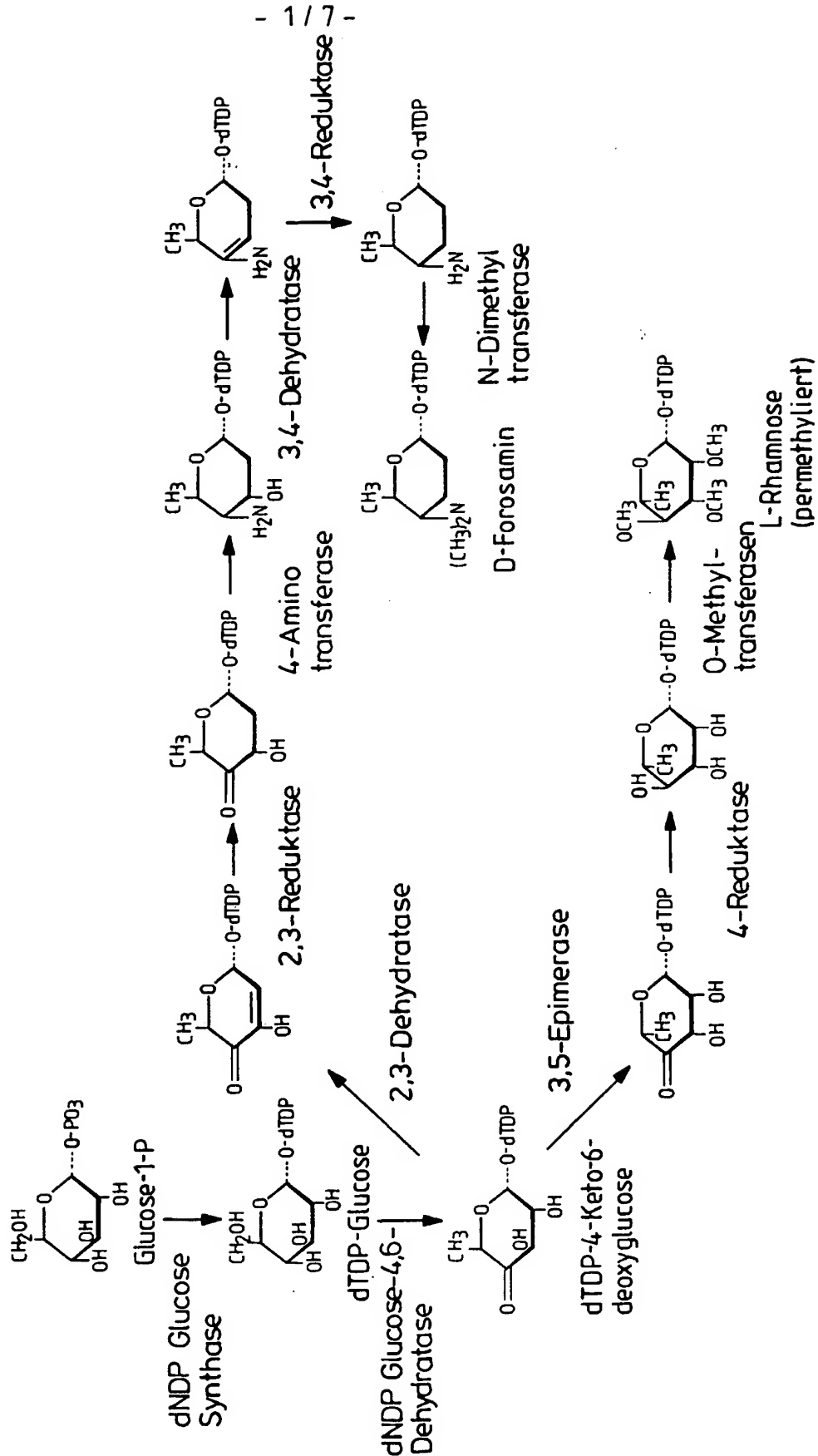
Fig. 2

Lage, der an der Spinosyn Biosynthese direkt oder indirekt beteiligten
DNA-Regionen 1 und 2 sowie Lage und Bezeichnung der zur
Sequenzierung herangezogenen überlappenden Cosmidklone

DNA-Regionen

SEQ ID NO. 1, 2 und 3

DNA-Region 1 (SEQ ID NO. 4)   DNA-Region 2 (SEQ ID NO. 5 und 6)

DNA-Größen Skala (kb)

50 40 30 20 10 0 10 20 30 40 50 60 70 80
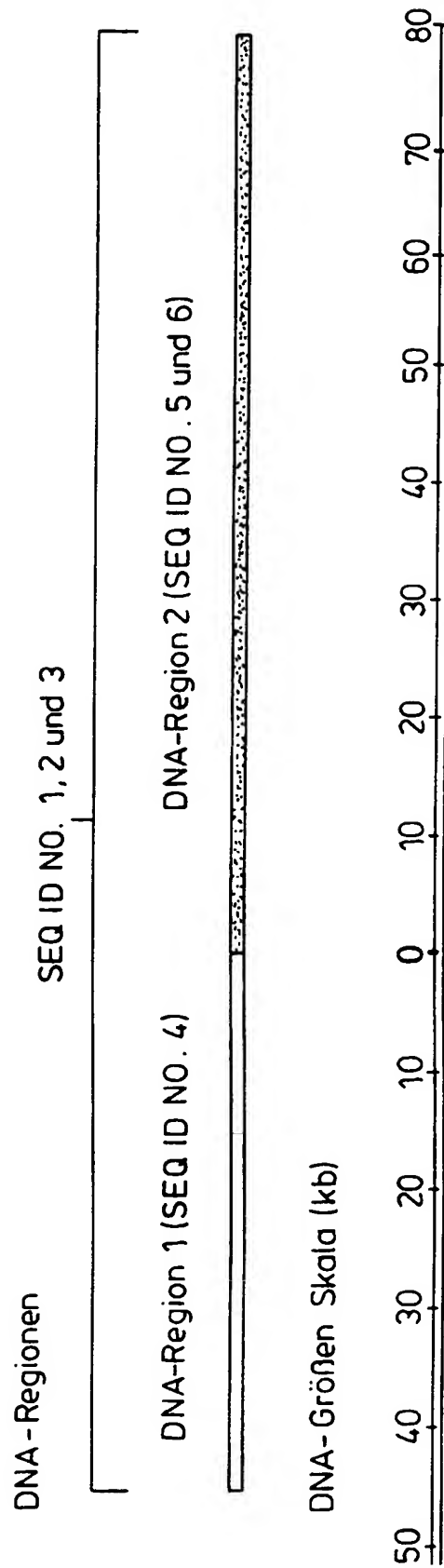
Cosmid-Bezeichnung, sowie Größe, Position und Überlappung von Insert-DNA

16-59-1

16-59-6

16-1-8

16-59-8
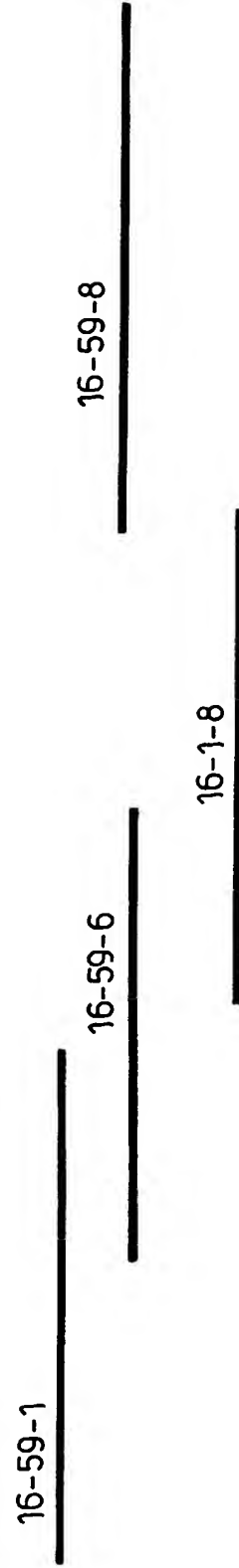
Fig. 3

Zur Biotransformation herangezogene Cosmidklone

DNA-Regionen

SEQ ID NO. 1,2 und 3

DNA-Region 1 (SEQ ID NO.4)   DNA-Region 2 (SEQ ID NO. 5 und 6)

DNA-Größen Skala (kb) und Position der ORF's 1 bis 22

Cosmid-Bezeichnung, sowie Größe und Position von Insert-DNA

165-1

165-8
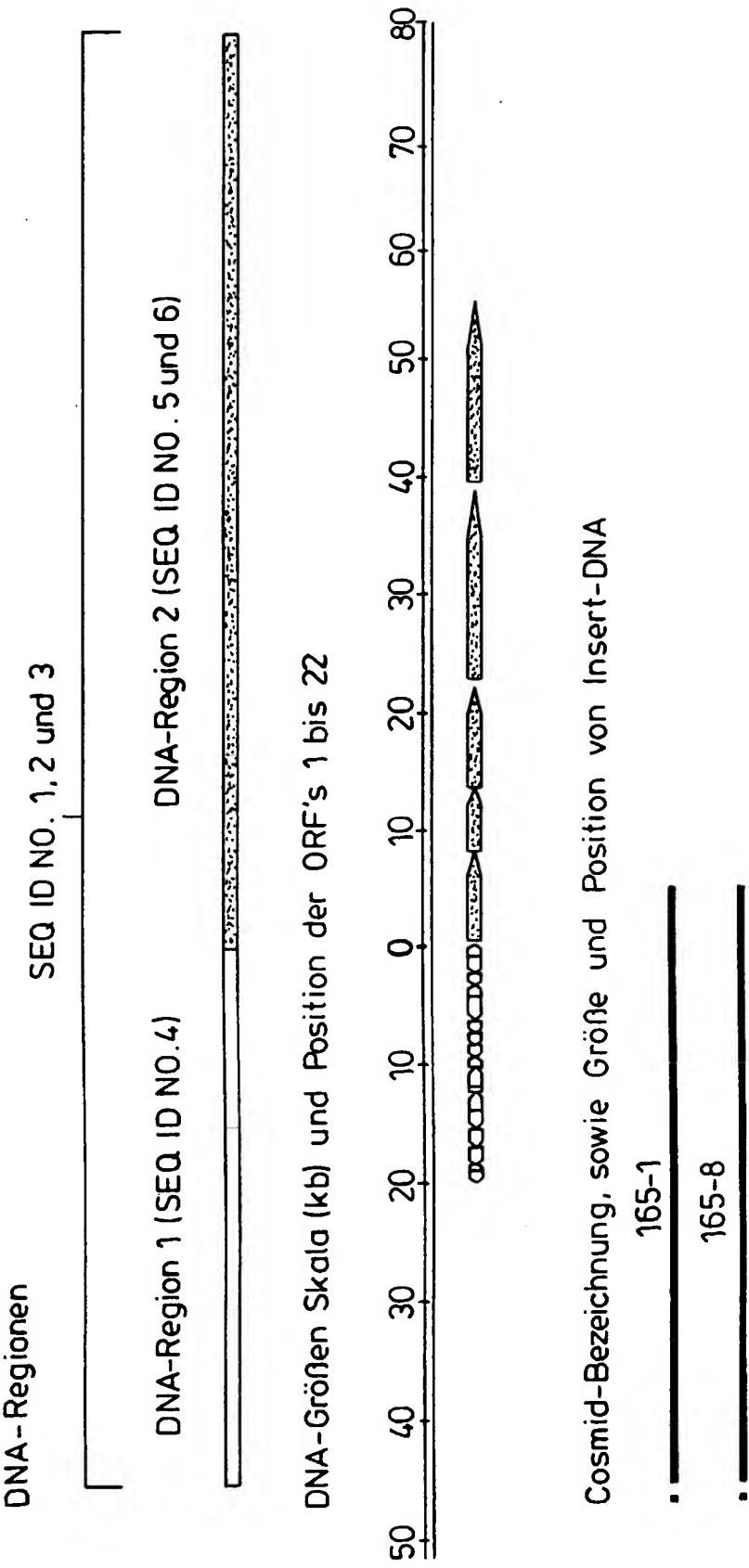
Fig. 4

Darstellung offener Leserahmen der
DNA-Region 3 (SEQ ID NO. 51) auf Cosmid 16-2-2

SEQ ID NO. 51

DNA-Größen Skala (kb) und Nukleotidposition

ORF24 (SEQ ID NO. 54)

ORF23 (SEQ ID NO. 52)
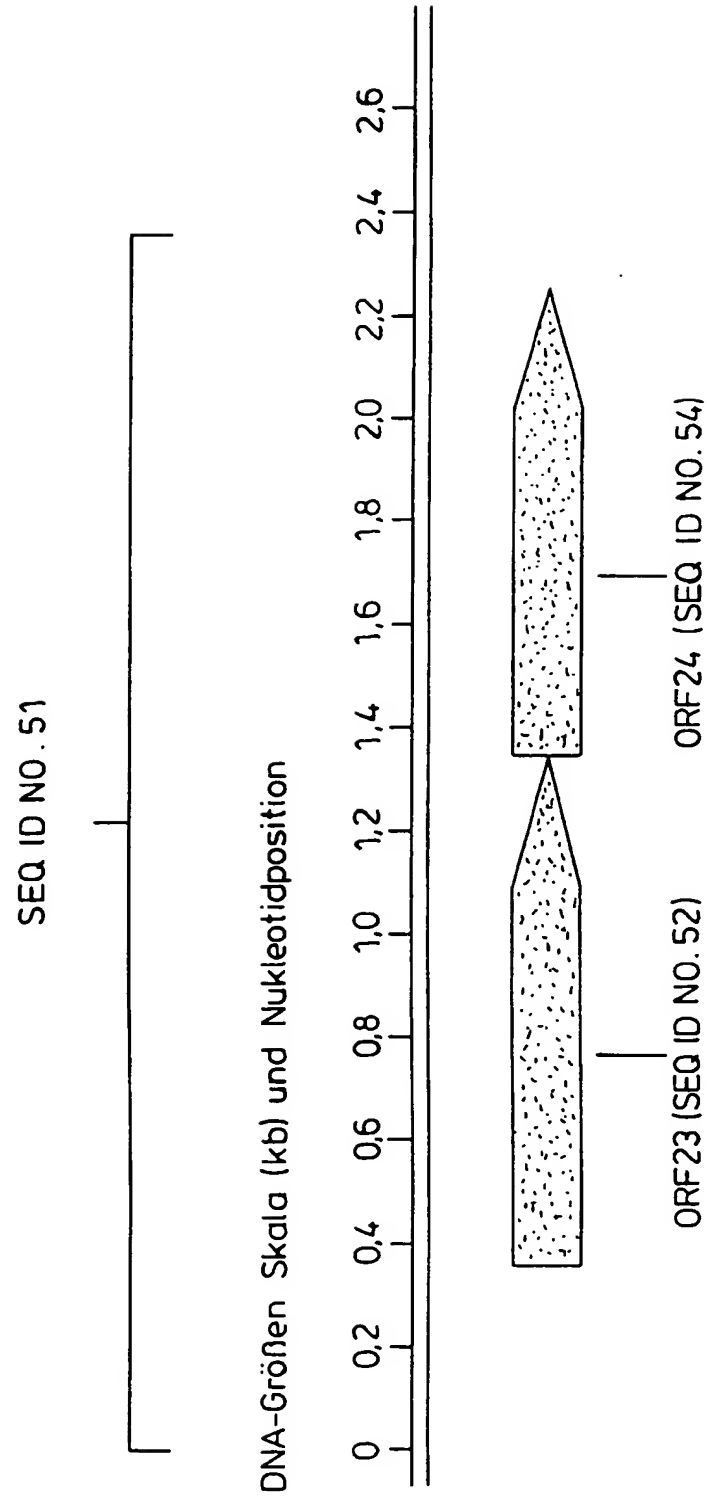
Fig. 5

Darstellung offener Leserahmen der DNA-Regionen 1 und 2, die
direkt oder indirekt an der Spinosyn-Biosynthese involviert sind

DNA-Region

DNA-Region 1 (Ausschnitt)   DNA-Region 2 (Ausschnitt)

DNA-Größen Skala (kb) und Nukleotidposition

Offene Leserahmen (ORF's)

ORF's 1 bis 17   ORF18 ORF19 ORF20   ORF 21   ORF 22
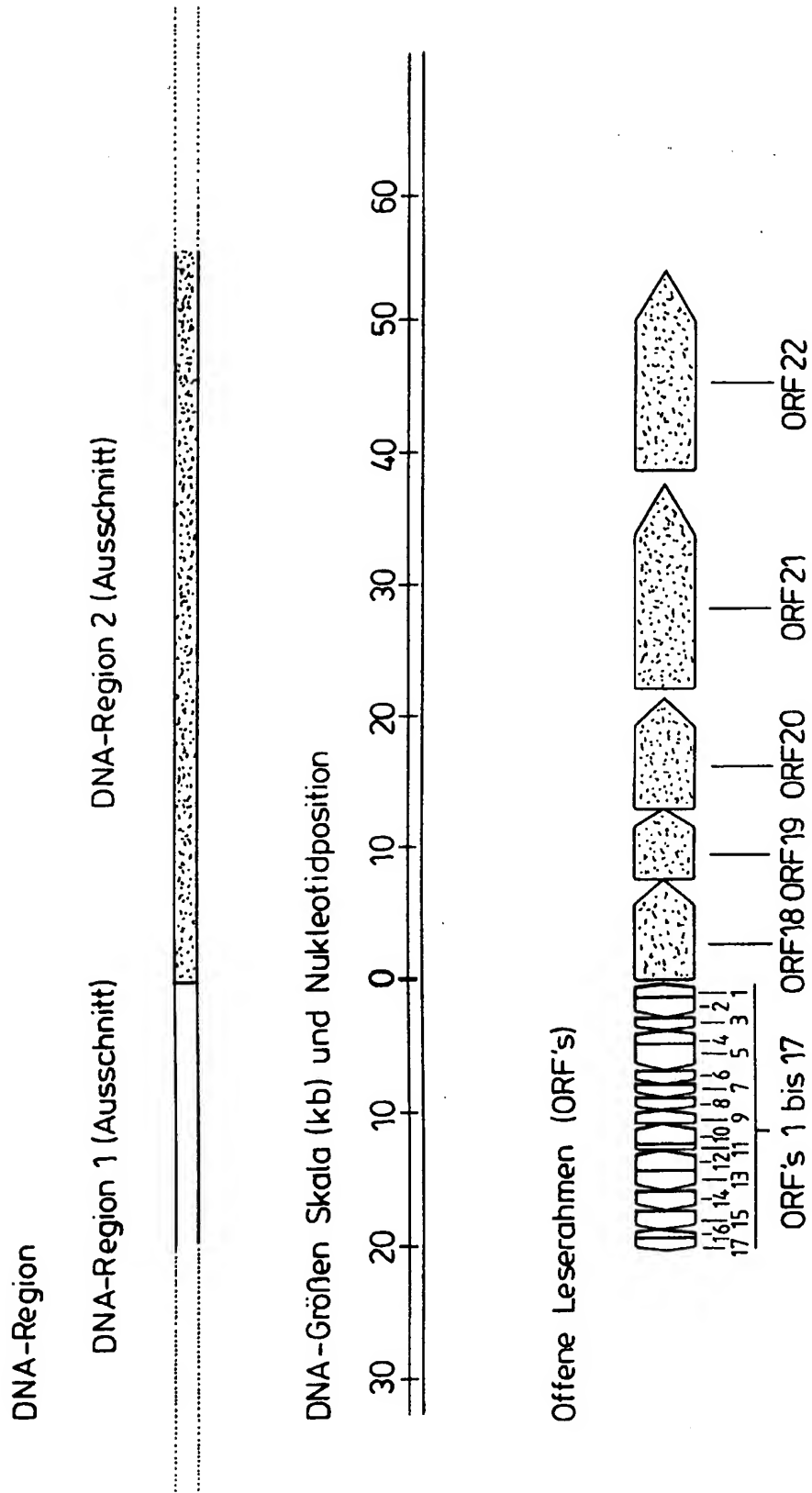
Fig. 6

Darstellung offener Leserahmen der DNA-Region 2
und ableitbare Polyketidsynthase-Module und Domänen

Module und Domänen

Offene Leserahmen
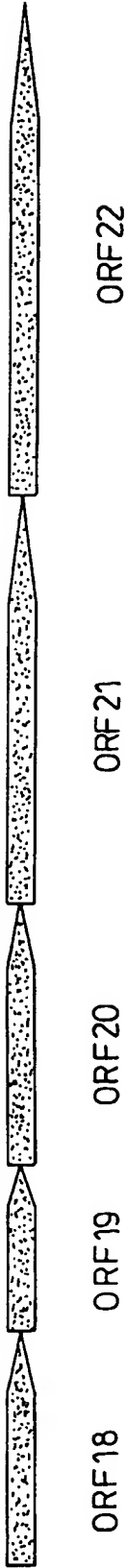
Fig. 7

Darstellung von Spinosyn Biosynthesegen BAC Shuttleklonen

DNA-Regionen

SEQ ID NO. 1, 2 und 3

DNA-Region 1 (SEQ ID NO.4)   DNA-Region 2 (SEQ ID NO. 5 und 6)

DNA-Größen Skala (kb) und Position der ORF's 1 bis 22

BAC Shuttleklon-Bezeichnung, sowie Größe und Position von Insert-DNA

P11/G6 (>100 kb)

P11/B10 (>100 kb)

P8/G11 (>100 kb)
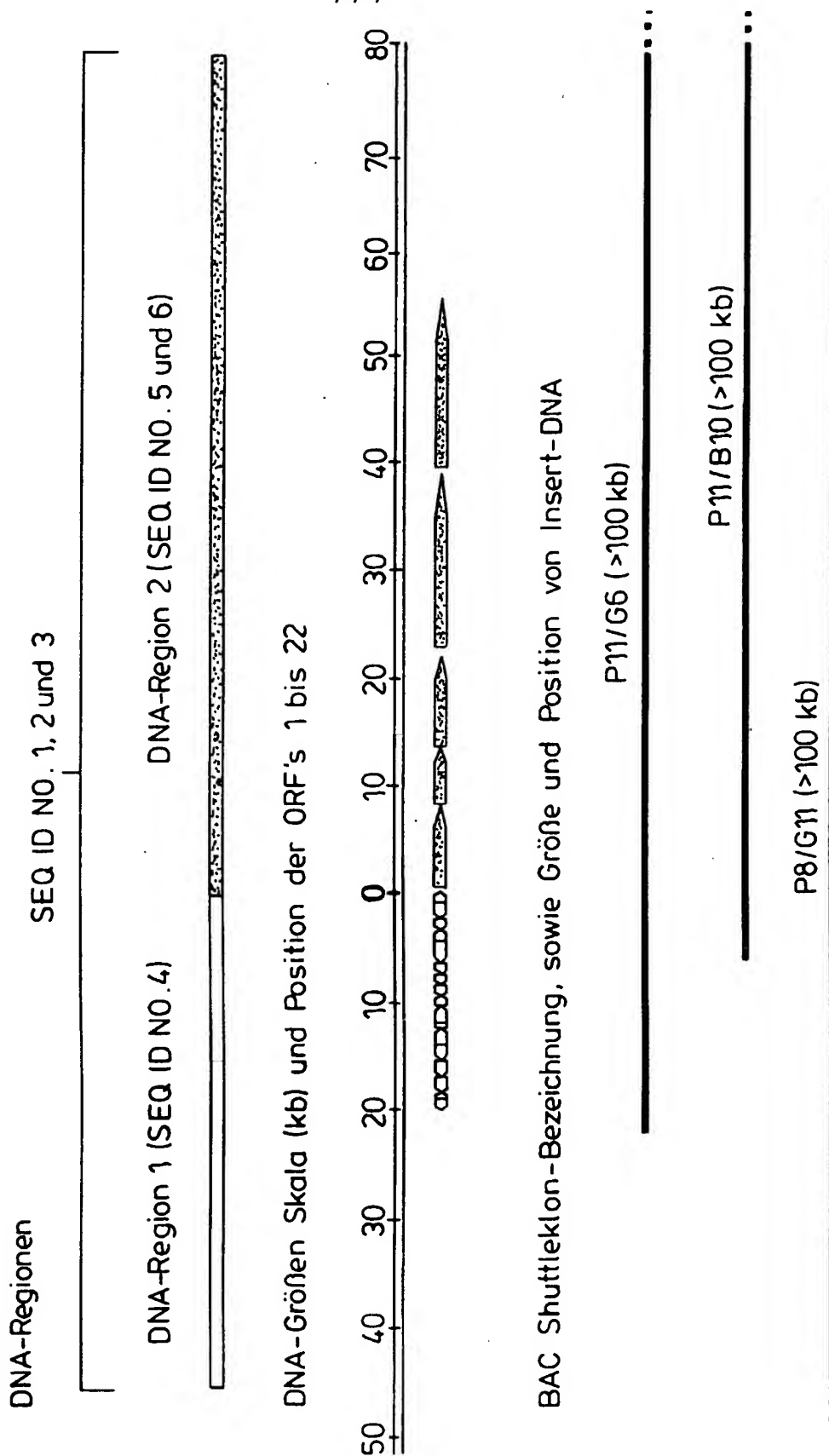
SEQUENZPROTOKOLL

<110> Bayer Aktiengesellschaft

<120> Nucleinsäuren, die für Enzymaktivitäten der
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<140>
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<150> DE 199 40 596.4
<151> 1999-08-27

<150> DE 199 57 268.2
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<210> 7
<211> 828
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(825)
<223> ORF1; O-Methyltransferase

<400> 7
gtg ttg cca ggt ggc gca cca aca tcg cag cag gtt ggg cag atg tat      48
Val Leu Pro Gly Gly Ala Pro Thr Ser Gln Gln Val Gly Gln Met Tyr
 1               5                  10                  15


gac ctg gtc acg ccg ttg ctg aac tcg gtc gcg ggc ggc ccc tgc gcc      96
Asp Leu Val Thr Pro Leu Leu Asn Ser Val Ala Gly Gly Pro Cys Ala
                20                  25                  30


atc cac cac ggc tac tgg gag aac gac ggg cgg gct tcc tgg cag cag     144
```

```
Ile His His Gly Tyr Trp Glu Asn Asp Gly Arg Ala Ser Trp Gln Gln
        35                40                45

gcc gcc gac cgg ctc acc gac ctt gtc gcc gaa cgg acc gtg ctc gat    192
Ala Ala Asp Arg Leu Thr Asp Leu Val Ala Glu Arg Thr Val Leu Asp
        50                55                60

ggc ggc gtt cga ctg ctc gat gtg ggg tgc ggt acc gga caa cca gcg    240
Gly Gly Val Arg Leu Leu Asp Val Gly Cys Gly Thr Gly Gln Pro Ala
65              70                75                80

ctg cgc gtc gcg cgc gac aac gcg atc cag atc acc ggc atc acc gtc    288
Leu Arg Val Ala Arg Asp Asn Ala Ile Gln Ile Thr Gly Ile Thr Val
                85                90                95

agc cag gtg caa gtg gcc atc gcc gct gat tgc gca cgc gaa cgc gga    336
Ser Gln Val Gln Val Ala Ile Ala Ala Asp Cys Ala Arg Glu Arg Gly
                100               105               110

cta agc cac cgg gtg gac ttc tcg tgc gtc gat gcc atg tcc ctg ccg    384
Leu Ser His Arg Val Asp Phe Ser Cys Val Asp Ala Met Ser Leu Pro
            115               120               125

tac ccg gac aat gct ttc gac gcc gcc tgg gcc atg cag tcg ctg ttg    432
Tyr Pro Asp Asn Ala Phe Asp Ala Ala Trp Ala Met Gln Ser Leu Leu
        130               135               140

gag atg tcc gaa ccg gac cgt gcc atc cgg gaa atc ctt cga gta ctc    480
Glu Met Ser Glu Pro Asp Arg Ala Ile Arg Glu Ile Leu Arg Val Leu
145               150               155               160

aaa ccc ggt ggc atc ctc ggc gtc acc gag gtc gtc aaa cga gaa gcg    528
Lys Pro Gly Gly Ile Leu Gly Val Thr Glu Val Val Lys Arg Glu Ala
                165               170               175

ggc ggc ggg atg ccg gtg tcc ggg gac agg tgg ccg acc ggc ctt cgg    576
Gly Gly Gly Met Pro Val Ser Gly Asp Arg Trp Pro Thr Gly Leu Arg
                180               185               190

atc tgc ctg gct gag caa ctt ctg gaa tcg ctg cgt gca gcg ggg ttc    624
Ile Cys Leu Ala Glu Gln Leu Leu Glu Ser Leu Arg Ala Ala Gly Phe
            195               200               205

gag atc ctc gat tgg gag gac gtg tcg tcg agg acc cgg tac ttc atg    672
Glu Ile Leu Asp Trp Glu Asp Val Ser Ser Arg Thr Arg Tyr Phe Met
        210               215               220

ccg cag ttc gcc gaa gag ctc gct gcg cac cag cac ggg atc gcg gac    720
```

·90

```
Pro Gln Phe Ala Glu Glu Leu Ala Ala His Gln His Gly Ile Ala Asp
225             230             235             240


agg tac ggg ccg gct gtc gcc ggc tgg gcc gcc gcg gtc tgc gat tat   768
Arg Tyr Gly Pro Ala Val Ala Gly Trp Ala Ala Ala Val Cys Asp Tyr
                245             250             255


gag aaa tat gcc cac gac atg ggc tat gcg att ctg acg gcg cgg aag   816
Glu Lys Tyr Ala His Asp Met Gly Tyr Ala Ile Leu Thr Ala Arg Lys
                260             265             270


ccg gtc ggc tga                                                   828
Pro Val Gly
        275
```

```
<210> 8
<211> 275
<212> PRT
<213> Saccharopolyspora spinosa

<400> 8
Val Leu Pro Gly Gly Ala Pro Thr Ser Gln Gln Val Gly Gln Met Tyr
1               5               10              15


Asp Leu Val Thr Pro Leu Leu Asn Ser Val Ala Gly Gly Pro Cys Ala
            20              25              30


Ile His His Gly Tyr Trp Glu Asn Asp Gly Arg Ala Ser Trp Gln Gln
        35              40              45


Ala Ala Asp Arg Leu Thr Asp Leu Val Ala Glu Arg Thr Val Leu Asp
    50              55              60


Gly Gly Val Arg Leu Leu Asp Val Gly Cys Gly Thr Gly Gln Pro Ala
65              70              75              80


Leu Arg Val Ala Arg Asp Asn Ala Ile Gln Ile Thr Gly Ile Thr Val
                85              90              95


Ser Gln Val Gln Val Ala Ile Ala Ala Asp Cys Ala Arg Glu Arg Gly
            100             105             110


Leu Ser His Arg Val Asp Phe Ser Cys Val Asp Ala Met Ser Leu Pro
        115             120             125


Tyr Pro Asp Asn Ala Phe Asp Ala Ala Trp Ala Met Gln Ser Leu Leu
        130             135             140
```

```
Glu Met Ser Glu Pro Asp Arg Ala Ile Arg Glu Ile Leu Arg Val Leu
145                 150             155             160

Lys Pro Gly Gly Ile Leu Gly Val Thr Glu Val Val Lys Arg Glu Ala
            165             170             175

Gly Gly Gly Met Pro Val Ser Gly Asp Arg Trp Pro Thr Gly Leu Arg
            180             185             190

Ile Cys Leu Ala Glu Gln Leu Leu Glu Ser Leu Arg Ala Ala Gly Phe
            195             200             205

Glu Ile Leu Asp Trp Glu Asp Val Ser Ser Arg Thr Arg Tyr Phe Met
    210             215             220

Pro Gln Phe Ala Glu Glu Leu Ala Ala His Gln His Gly Ile Ala Asp
225             230                 235             240

Arg Tyr Gly Pro Ala Val Ala Gly Trp Ala Ala Ala Val Cys Asp Tyr
            245             250             255

Glu Lys Tyr Ala His Asp Met Gly Tyr Ala Ile Leu Thr Ala Arg Lys
            260             265             270

Pro Val Gly
        275
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```
<400> 9
atg cgc gta ctc gtc gtt ccc ttg ccc tat ccg acg cat ctc atg gca    48
Met Arg Val Leu Val Val Pro Leu Pro Tyr Pro Thr His Leu Met Ala
  1               5                   10                  15

atg gtg ccg ctg tgc tgg gcg ctg caa gca tcc ggg cac gag gtc ctg    96
Met Val Pro Leu Cys Trp Ala Leu Gln Ala Ser Gly His Glu Val Leu
              20                  25                  30
```

atc gcc gca cca cca gag ctg cag gcg acc gcg cat ggt gca ggt ctc   144
Ile Ala Ala Pro Pro Glu Leu Gln Ala Thr Ala His Gly Ala Gly Leu
            35   40   45

acc acg gcc ggg atc cgc ggg aac gac agg acc ggc gat acg ggt gga   192
Thr Thr Ala Gly Ile Arg Gly Asn Asp Arg Thr Gly Asp Thr Gly Gly
        50   55   60

acc acg cag ctg cgc ttt ccc aat ccg gcg ttc ggt cag cgc gac acc   240
Thr Thr Gln Leu Arg Phe Pro Asn Pro Ala Phe Gly Gln Arg Asp Thr
65   70   75   80

gag gca ggc cgg caa ctg tgg gag cag acc gcg tcc aat gtc gcg caa   288
Glu Ala Gly Arg Gln Leu Trp Glu Gln Thr Ala Ser Asn Val Ala Gln
                85   90   95

agc tcg ctc gat cag ctc ccc gaa tac ctt cga ctg gcc gag gcc tgg   336
Ser Ser Leu Asp Gln Leu Pro Glu Tyr Leu Arg Leu Ala Glu Ala Trp
            100   105   110

cga ccg tca gtg ctg ttg gtc gac gtc tgc gcg ctg atc ggc cgg gtg   384
Arg Pro Ser Val Leu Leu Val Asp Val Cys Ala Leu Ile Gly Arg Val
            115   120   125

ctc ggc gga ttg ctc gac ctg ccg gtc gtg ctg cac cgc tgg gga gtc   432
Leu Gly Gly Leu Leu Asp Leu Pro Val Val Leu His Arg Trp Gly Val
        130   135   140

gac ccc acc gca ggc ccc ttc agc gat cga gcc cac gag ttg ctt gac   480
Asp Pro Thr Ala Gly Pro Phe Ser Asp Arg Ala His Glu Leu Leu Asp
145   150   155   160

ccg gtg tgc cgg cac cac gga ctg acc ggc ctg ccc act ccc gag ctc   528
Pro Val Cys Arg His His Gly Leu Thr Gly Leu Pro Thr Pro Glu Leu
            165   170   175

atc ctc gat ccc tgt ccg ccg agc ctg caa gca agc gac gcg ccg caa   576
Ile Leu Asp Pro Cys Pro Pro Ser Leu Gln Ala Ser Asp Ala Pro Gln
            180   185   190

ggc gca ccg gtc cag tac gtg ccg tac aac gga agc ggc gca ttc ccg   624
Gly Ala Pro Val Gln Tyr Val Pro Tyr Asn Gly Ser Gly Ala Phe Pro
        195   200   205

gca tgg ggc gcg gcg cgc acc tca gca cgg cgg gtc tgc atc tgc atg   672
Ala Trp Gly Ala Ala Arg Thr Ser Ala Arg Arg Val Cys Ile Cys Met
        210   215   220

```
ggc cgc atg gtg ctg aac gcc acc ggg ccg gct ccg ctg ctg cgc gca    720
Gly Arg Met Val Leu Asn Ala Thr Gly Pro Ala Pro Leu Leu Arg Ala
225                 230             235             240

gta gcg gct gcc acc gag ttg ccc ggc gtc gag gcc gtg atc gcc gtt    768
Val Ala Ala Ala Thr Glu Leu Pro Gly Val Glu Ala Val Ile Ala Val
                245             250             255

ccc ccc gag cac cgg gca ctt ctc acc gac cta ccc gac aac gcc cgg    816
Pro Pro Glu His Arg Ala Leu Leu Thr Asp Leu Pro Asp Asn Ala Arg
                260             265             270

atc gcc gaa tcg gtc ccg ctc aac ctg ttc ctg cgt acc tgc gag ctg    864
Ile Ala Glu Ser Val Pro Leu Asn Leu Phe Leu Arg Thr Cys Glu Leu
                275             280             285

gtc atc tgc gcg ggc ggc tcg gga acg gca ttc acc gcg acc cga ctc    912
Val Ile Cys Ala Gly Gly Ser Gly Thr Ala Phe Thr Ala Thr Arg Leu
                290             295             300

ggc atc ccg caa ctc gtg ctt ccc cag tac ttc gac cag ttc gac tac    960
Gly Ile Pro Gln Leu Val Leu Pro Gln Tyr Phe Asp Gln Phe Asp Tyr
305                 310             315             320

gcg cgc aac ctc gcc gct gcc ggg gcg ggc atc tgc ttg ccg gat gag    1008
Ala Arg Asn Leu Ala Ala Ala Gly Ala Gly Ile Cys Leu Pro Asp Glu
                325             330             335

cag gcc cag tcc gac cac gaa cag ttc acc gac tca atc gca acg gtg    1056
Gln Ala Gln Ser Asp His Glu Gln Phe Thr Asp Ser Ile Ala Thr Val
                340             345             350

ctc ggc gac acc ggc ttc gct gct gcg gca atc aaa ctc agc gac gag    1104
Leu Gly Asp Thr Gly Phe Ala Ala Ala Ala Ile Lys Leu Ser Asp Glu
                355             360             365

atc acg gcc atg ccc cat ccc gcc gcg ctg gtg cgg acg ctg gag aac    1152
Ile Thr Ala Met Pro His Pro Ala Ala Leu Val Arg Thr Leu Glu Asn
                370             375             380

act gcg gcc atc cgt gcc tga                                         1173
Thr Ala Ala Ile Arg Ala
385                 390
```

```
<210> 10
<211> 390
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<212> PRT
<213> Saccharopolyspora spinosa

<400> 10
Met Arg Val Leu Val Val Pro Leu Pro Tyr Pro Thr His Leu Met Ala
1   5   10   15

Met Val Pro Leu Cys Trp Ala Leu Gln Ala Ser Gly His Glu Val Leu
            20   25   30

Ile Ala Ala Pro Pro Glu Leu Gln Ala Thr Ala His Gly Ala Gly Leu
        35   40   45

Thr Thr Ala Gly Ile Arg Gly Asn Asp Arg Thr Gly Asp Thr Gly Gly
    50   55   60

Thr Thr Gln Leu Arg Phe Pro Asn Pro Ala Phe Gly Gln Arg Asp Thr
65   70   75   80

Glu Ala Gly Arg Gln Leu Trp Glu Gln Thr Ala Ser Asn Val Ala Gln
            85   90   95

Ser Ser Leu Asp Gln Leu Pro Glu Tyr Leu Arg Leu Ala Glu Ala Trp
            100   105   110

Arg Pro Ser Val Leu Leu Val Asp Val Cys Ala Leu Ile Gly Arg Val
        115   120   125

Leu Gly Gly Leu Leu Asp Leu Pro Val Val Leu His Arg Trp Gly Val
    130   135   140

Asp Pro Thr Ala Gly Pro Phe Ser Asp Arg Ala His Glu Leu Leu Asp
145   150   155   160

Pro Val Cys Arg His His Gly Leu Thr Gly Leu Pro Thr Pro Glu Leu
            165   170   175

Ile Leu Asp Pro Cys Pro Pro Ser Leu Gln Ala Ser Asp Ala Pro Gln
            180   185   190

Gly Ala Pro Val Gln Tyr Val Pro Tyr Asn Gly Ser Gly Ala Phe Pro
        195   200   205

Ala Trp Gly Ala Ala Arg Thr Ser Ala Arg Arg Val Cys Ile Cys Met
    210   215   220

Gly Arg Met Val Leu Asn Ala Thr Gly Pro Ala Pro Leu Leu Arg Ala
225   230   235   240

95

```
Val Ala Ala Ala Thr Glu Leu Pro Gly Val Glu Ala Val Ile Ala Val
              245               250           255

Pro Pro Glu His Arg Ala Leu Leu Thr Asp Leu Pro Asp Asn Ala Arg
          260                265           270

Ile Ala Glu Ser Val Pro Leu Asn Leu Phe Leu Arg Thr Cys Glu Leu
          275               280           285

Val Ile Cys Ala Gly Gly Ser Gly Thr Ala Phe Thr Ala Thr Arg Leu
          290               295           300

Gly Ile Pro Gln Leu Val Leu Pro Gln Tyr Phe Asp Gln Phe Asp Tyr
305               310               315               320

Ala Arg Asn Leu Ala Ala Ala Gly Ala Gly Ile Cys Leu Pro Asp Glu
              325               330               335

Gln Ala Gln Ser Asp His Glu Gln Phe Thr Asp Ser Ile Ala Thr Val
          340               345           350

Leu Gly Asp Thr Gly Phe Ala Ala Ala Ala Ile Lys Leu Ser Asp Glu
          355               360           365

Ile Thr Ala Met Pro His Pro Ala Ala Leu Val Arg Thr Leu Glu Asn
370               375               380

Thr Ala Ala Ile Arg Ala
385               390
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<210> 11
<211> 753
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(750)
<223> ORF3; O-Methyltransferase

<400> 11
atg ccc tcc cag aac gcg ctg tac ctg gac ctg ctc aag aag gta ctc     48
Met Pro Ser Gln Asn Ala Leu Tyr Leu Asp Leu Leu Lys Lys Val Leu
  1               5                  10                  15
```

```
acc aac acg att tac agt gat cgg ccg cat ccg aac gcc tgg cag gac    96
Thr Asn Thr Ile Tyr Ser Asp Arg Pro His Pro Asn Ala Trp Gln Asp
            20                  25                  30

aac acc gac tac agg cag gcc gct cgg gcc aaa ggc acg gac tgg cca   144
Asn Thr Asp Tyr Arg Gln Ala Ala Arg Ala Lys Gly Thr Asp Trp Pro
            35                  40                  45

act gtc gcg cac acg atg atc ggt ctg gag cgg ctg gac aac ctc cag   192
Thr Val Ala His Thr Met Ile Gly Leu Glu Arg Leu Asp Asn Leu Gln
            50                  55                  60

cac tgc gtg gaa gcc gtg ctc gca gac ggt gtt ccc ggg gat ttc gcc   240
His Cys Val Glu Ala Val Leu Ala Asp Gly Val Pro Gly Asp Phe Ala
65                  70                  75                  80

gag acc ggt gtc tgg cgg ggc ggc gca tgc atc ttc atg cgc gcg gtt   288
Glu Thr Gly Val Trp Arg Gly Gly Ala Cys Ile Phe Met Arg Ala Val
            85                  90                  95

ctc cag gca ttc gga gat acc gga cgt acc gtc tgg gta gtg gat tcc   336
Leu Gln Ala Phe Gly Asp Thr Gly Arg Thr Val Trp Val Val Asp Ser
            100                 105                 110

ttc cag gga atg ccg gaa agc tct gcg caa gac cac caa gcg gac cag   384
Phe Gln Gly Met Pro Glu Ser Ser Ala Gln Asp His Gln Ala Asp Gln
            115                 120                 125

gct atg gcg ctg cac gag tac aac gac gtg ctt ggc gta tcg ctt gag   432
Ala Met Ala Leu His Glu Tyr Asn Asp Val Leu Gly Val Ser Leu Glu
            130                 135                 140

acc gtc cgg cag aac ttc gcc cgc tac ggg ctg ctc gac gaa cag gtc   480
Thr Val Arg Gln Asn Phe Ala Arg Tyr Gly Leu Leu Asp Glu Gln Val
145                 150                 155                 160

agg ttc ctc ccc ggc tgg ttc cgg gac acc ttg ccc acc gcc ccc atc   528
Arg Phe Leu Pro Gly Trp Phe Arg Asp Thr Leu Pro Thr Ala Pro Ile
            165                 170                 175

cag gaa ctc gcc gtg cta cga ctc gac ggc gac ctc tac gaa tcc aca   576
Gln Glu Leu Ala Val Leu Arg Leu Asp Gly Asp Leu Tyr Glu Ser Thr
            180                 185                 190

atg gac tca ttg cgg aac ctg tac ccg aag ctc tcg ccg ggc gga ttc   624
Met Asp Ser Leu Arg Asn Leu Tyr Pro Lys Leu Ser Pro Gly Gly Phe
            195                 200                 205
```

```
gtc atc atc gac gac tat ttt ctg ccg tcc tgc cag gac gcg gtg aag    672
Val Ile Ile Asp Asp Tyr Phe Leu Pro Ser Cys Gln Asp Ala Val Lys
    210             215             220

ggg ttc cgc gcg gaa ctc ggg atc acg gaa ccc atc cac gac atc gac    720
Gly Phe Arg Ala Glu Leu Gly Ile Thr Glu Pro Ile His Asp Ile Asp
225             230             235             240

ggc acg ggc gcc tac tgg cgc cgc agc tgg tga                        753
Gly Thr Gly Ala Tyr Trp Arg Arg Ser Trp
                245             250
```

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<210> 12
<211> 250
<212> PRT
<213> Saccharopolyspora spinosa

<400> 12
Met Pro Ser Gln Asn Ala Leu Tyr Leu Asp Leu Leu Lys Lys Val Leu
1               5               10              15

Thr Asn Thr Ile Tyr Ser Asp Arg Pro His Pro Asn Ala Trp Gln Asp
            20              25              30

Asn Thr Asp Tyr Arg Gln Ala Ala Arg Ala Lys Gly Thr Asp Trp Pro
            35              40              45

Thr Val Ala His Thr Met Ile Gly Leu Glu Arg Leu Asp Asn Leu Gln
        50              55              60

His Cys Val Glu Ala Val Leu Ala Asp Gly Val Pro Gly Asp Phe Ala
65              70              75              80

Glu Thr Gly Val Trp Arg Gly Gly Ala Cys Ile Phe Met Arg Ala Val
                85              90              95

Leu Gln Ala Phe Gly Asp Thr Gly Arg Thr Val Trp Val Val Asp Ser
            100             105             110

Phe Gln Gly Met Pro Glu Ser Ser Ala Gln Asp His Gln Ala Asp Gln
        115             120             125

Ala Met Ala Leu His Glu Tyr Asn Asp Val Leu Gly Val Ser Leu Glu
        130             135             140

Thr Val Arg Gln Asn Phe Ala Arg Tyr Gly Leu Leu Asp Glu Gln Val
145             150             155             160
```

```
Arg Phe Leu Pro Gly Trp Phe Arg Asp Thr Leu Pro Thr Ala Pro Ile
            165             170             175

Gln Glu Leu Ala Val Leu Arg Leu Asp Gly Asp Leu Tyr Glu Ser Thr
            180             185             190

Met Asp Ser Leu Arg Asn Leu Tyr Pro Lys Leu Ser Pro Gly Gly Phe
            195             200             205

Val Ile Ile Asp Asp Tyr Phe Leu Pro Ser Cys Gln Asp Ala Val Lys
    210             215             220

Gly Phe Arg Ala Glu Leu Gly Ile Thr Glu Pro Ile His Asp Ile Asp
225             230             235             240

Gly Thr Gly Ala Tyr Trp Arg Arg Ser Trp
            245             250
```

<210> 13
<211> 1188
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(1185)
<223> ORF4; O-Methyltransferase

<400> 13

```
atg agt gag atc gca gtt gcc ccc tgg tcg gtg gtg gag cgt ttg ctg   48
Met Ser Glu Ile Ala Val Ala Pro Trp Ser Val Val Glu Arg Leu Leu
 1               5                  10                  15

ctc gcg gcg ggt gcg ggc ccg gcg aag ctc cag gaa gca gtg cag gtg   96
Leu Ala Ala Gly Ala Gly Pro Ala Lys Leu Gln Glu Ala Val Gln Val
            20                  25                  30

gcc gga ctg gac gcg gtg gcc gac gcc atc gtc gac gaa ctc gtc gta  144
Ala Gly Leu Asp Ala Val Ala Asp Ala Ile Val Asp Glu Leu Val Val
            35                  40                  45

cgc tgc gat ccg ctg tcg ttg gac gag tcg gtg cga atc ggc ctg gag  192
Arg Cys Asp Pro Leu Ser Leu Asp Glu Ser Val Arg Ile Gly Leu Glu
    50                  55                  60
```

99

```
atc act tct ggc gct cag ctg gtc cgg aga acc gtt gag ctc gat cac    240
Ile Thr Ser Gly Ala Gln Leu Val Arg Arg Thr Val Glu Leu Asp His
65              70              75              80


gca ggc ctg cgg ctc gcg gcg gtc gcc gaa gca gct gct gtt ctc cgg    288
Ala Gly Leu Arg Leu Ala Ala Val Ala Glu Ala Ala Ala Val Leu Arg
                85              90              95


ttc gac gcg gtg gat ctg ctg gaa ggg ctc ttc ggc ccg gtt gac ggc    336
Phe Asp Ala Val Asp Leu Leu Glu Gly Leu Phe Gly Pro Val Asp Gly
                100             105             110


agg cgg cac aac agc cgt gaa gtc cgc tgg tcg gac agc atg acg cag    384
Arg Arg His Asn Ser Arg Glu Val Arg Trp Ser Asp Ser Met Thr Gln
                115             120             125


ttc tcg ccc gac cag ggc ctc gcc ggc gcg cag cgc ctg ctg gcg ttc    432
Phe Ser Pro Asp Gln Gly Leu Ala Gly Ala Gln Arg Leu Leu Ala Phe
                130             135             140


cgg aac agg gtg tcc acc gcg gtg cac gcc gtg ctg gcc gca gcc gcc    480
Arg Asn Arg Val Ser Thr Ala Val His Ala Val Leu Ala Ala Ala Ala
145             150             155             160


acc agg cgc gcg gac ctc ggt gcg ctg gca gtc cgc tac gga tcc gac    528
Thr Arg Arg Ala Asp Leu Gly Ala Leu Ala Val Arg Tyr Gly Ser Asp
                165             170             175


aaa tgg gcg gac ctg cac tgg tac acc gaa cac tac gag cac cac ttc    576
Lys Trp Ala Asp Leu His Trp Tyr Thr Glu His Tyr Glu His His Phe
                180             185             190


tcc cga ttc cag gat gcc ccg gtg cga gtg ttg gaa ata gga atc ggt    624
Ser Arg Phe Gln Asp Ala Pro Val Arg Val Leu Glu Ile Gly Ile Gly
                195             200             205


ggt tat cac gca ccc gaa ctc ggt ggt gct tcg ctg cgc atg tgg cag    672
Gly Tyr His Ala Pro Glu Leu Gly Gly Ala Ser Leu Arg Met Trp Gln
210             215             220


cgg tac ttc cgg cga ggt ctc gtt tac ggg ctg gac att ttc gag aaa    720
Arg Tyr Phe Arg Arg Gly Leu Val Tyr Gly Leu Asp Ile Phe Glu Lys
225             230             235             240


gcc ggg aac gaa ggg cac cga gtg cga aag ctg cga ggt gac cag agc    768
Ala Gly Asn Glu Gly His Arg Val Arg Lys Leu Arg Gly Asp Gln Ser
                245             250             255
```

```
gat gcg gaa ttc ctg gaa gac atg gcg ggg aag atc ggg ccg ttc gac    816
Asp Ala Glu Phe Leu Glu Asp Met Ala Gly Lys Ile Gly Pro Phe Asp
            260             265             270

att gtc atc gac gac ggc agc cat gtc aac gac cac gtc aag aaa tcc    864
Ile Val Ile Asp Asp Gly Ser His Val Asn Asp His Val Lys Lys Ser
            275             280             285

ttc caa tcc ctg ttt ccg cac gtc cgc cca ggt ggt ttg tac gtc atc    912
Phe Gln Ser Leu Phe Pro His Val Arg Pro Gly Gly Leu Tyr Val Ile
            290             295             300

gag gat ctc cag acg gcg tac tgg ccc ggc tac ggc ggt cgc gat ggg    960
Glu Asp Leu Gln Thr Ala Tyr Trp Pro Gly Tyr Gly Gly Arg Asp Gly
305             310             315             320

gaa ccc gcg gcc cag cgc acc tcg atc gac atg ctc aaa gaa ctg atc   1008
Glu Pro Ala Ala Gln Arg Thr Ser Ile Asp Met Leu Lys Glu Leu Ile
            325             330             335

gac ggc ctg cat tat cag gag cgc gaa tcg cgg tgc ggg acc gag ccc   1056
Asp Gly Leu His Tyr Gln Glu Arg Glu Ser Arg Cys Gly Thr Glu Pro
            340             345             350

tcc tac acg gaa cgg aac gtg gcg gcc ctg cac ttc tac cac aac ctg   1104
Ser Tyr Thr Glu Arg Asn Val Ala Ala Leu His Phe Tyr His Asn Leu
            355             360             365

gta ttc gtg gag aaa ggg ctc aac gct gag cct gcc gcg ccg ggg ttc   1152
Val Phe Val Glu Lys Gly Leu Asn Ala Glu Pro Ala Ala Pro Gly Phe
            370             375             380

gtg ccc cgg caa gcg ctc ggc gtc gag gac ggc tga                   1188
Val Pro Arg Gln Ala Leu Gly Val Glu Asp Gly
385             390             395
```

```
<210> 14
<211> 395
<212> PRT
<213> Saccharopolyspora spinosa

<400> 14
Met Ser Glu Ile Ala Val Ala Pro Trp Ser Val Val Glu Arg Leu Leu
1               5               10              15

Leu Ala Ala Gly Ala Gly Pro Ala Lys Leu Gln Glu Ala Val Gln Val
            20              25              30
```

```
Ala Gly Leu Asp Ala Val Ala Asp Ala Ile Val Asp Glu Leu Val Val
         35                  40                  45

Arg Cys Asp Pro Leu Ser Leu Asp Glu Ser Val Arg Ile Gly Leu Glu
         50                  55                  60

Ile Thr Ser Gly Ala Gln Leu Val Arg Arg Thr Val Glu Leu Asp His
65                  70                  75                  80

Ala Gly Leu Arg Leu Ala Ala Val Ala Glu Ala Ala Ala Val Leu Arg
                   85                  90                  95

Phe Asp Ala Val Asp Leu Leu Glu Gly Leu Phe Gly Pro Val Asp Gly
             100                 105                 110

Arg Arg His Asn Ser Arg Glu Val Arg Trp Ser Asp Ser Met Thr Gln
         115                 120                 125

Phe Ser Pro Asp Gln Gly Leu Ala Gly Ala Gln Arg Leu Leu Ala Phe
         130                 135                 140

Arg Asn Arg Val Ser Thr Ala Val His Ala Val Leu Ala Ala Ala Ala
145                 150                 155                 160

Thr Arg Arg Ala Asp Leu Gly Ala Leu Ala Val Arg Tyr Gly Ser Asp
                   165                 170                 175

Lys Trp Ala Asp Leu His Trp Tyr Thr Glu His Tyr Glu His His Phe
             180                 185                 190

Ser Arg Phe Gln Asp Ala Pro Val Arg Val Leu Glu Ile Gly Ile Gly
         195                 200                 205

Gly Tyr His Ala Pro Glu Leu Gly Gly Ala Ser Leu Arg Met Trp Gln
210                 215                 220

Arg Tyr Phe Arg Arg Gly Leu Val Tyr Gly Leu Asp Ile Phe Glu Lys
225                 230                 235                 240

Ala Gly Asn Glu Gly His Arg Val Arg Lys Leu Arg Gly Asp Gln Ser
             245                 250                 255

Asp Ala Glu Phe Leu Glu Asp Met Ala Gly Lys Ile Gly Pro Phe Asp
             260                 265                 270

Ile Val Ile Asp Asp Gly Ser His Val Asn Asp His Val Lys Lys Ser
         275                 280                 285
```

102

```
Phe Gln Ser Leu Phe Pro His Val Arg Pro Gly Gly Leu Tyr Val Ile
    290             295             300

Glu Asp Leu Gln Thr Ala Tyr Trp Pro Gly Tyr Gly Gly Arg Asp Gly
305             310             315             320

Glu Pro Ala Ala Gln Arg Thr Ser Ile Asp Met Leu Lys Glu Leu Ile
                325             330             335

Asp Gly Leu His Tyr Gln Glu Arg Glu Ser Arg Cys Gly Thr Glu Pro
            340             345             350

Ser Tyr Thr Glu Arg Asn Val Ala Ala Leu His Phe Tyr His Asn Leu
        355             360             365

Val Phe Val Glu Lys Gly Leu Asn Ala Glu Pro Ala Ala Pro Gly Phe
    370             375             380

Val Pro Arg Gln Ala Leu Gly Val Glu Asp Gly
385             390             395
```

<210> 15
<211> 1620
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(1617)
<223> ORF5; C-C verknüpfendes Enzym, Cyclisierungsenzym

<400> 15

```
atg atc tcg gct gcg ggc gaa caa agt gga cca gtc aga aaa gga ggg      48
Met Ile Ser Ala Ala Gly Glu Gln Ser Gly Pro Val Arg Lys Gly Gly
 1               5              10              15

gcg gtg ccc gaa ttc cat gac ccg gca ccc atg aat cgt cga acc cca      96
Ala Val Pro Glu Phe His Asp Pro Ala Pro Met Asn Arg Arg Thr Pro
                20              25              30

gga aca gag atc acc gtc gag ccc gac gat cct cgt tat ccg gac ctc     144
Gly Thr Glu Ile Thr Val Glu Pro Asp Asp Pro Arg Tyr Pro Asp Leu
            35              40              45

gtc gtc ggg cac aac ccc cgt ttc acc gga aaa ccc gaa cgc atc cac     192
```

```
Val Val Gly His Asn Pro Arg Phe Thr Gly Lys Pro Glu Arg Ile His
    50              55              60

atc gcc agc tcc gcc gaa gac gtc gtg cac gcc gtc gcc gac gcc gtg    240
Ile Ala Ser Ser Ala Glu Asp Val Val His Ala Val Ala Asp Ala Val
    65              70              75              80

cgc acc ggc agg cgg gta ggg gtc cgc agc ggc ggg cac tgc ttc gag    288
Arg Thr Gly Arg Arg Val Gly Val Arg Ser Gly Gly His Cys Phe Glu
                85              90              95

aat ctc gtt gcg gac ccg gcg atc cga gtg ctc gtc gac ctc tcc gag    336
Asn Leu Val Ala Asp Pro Ala Ile Arg Val Leu Val Asp Leu Ser Glu
            100             105             110

ctc aac cgc gtg tac tac gac agc acg cgc ggg gca ttc gcg atc gag    384
Leu Asn Arg Val Tyr Tyr Asp Ser Thr Arg Gly Ala Phe Ala Ile Glu
            115             120             125

gcg ggc gcc gcc ctc ggg cag gtg tac cga acc ctg ttc aag aac tgg    432
Ala Gly Ala Ala Leu Gly Gln Val Tyr Arg Thr Leu Phe Lys Asn Trp
    130             135             140

ggc gtg acg atc ccg acc ggc gca tgt ccc ggg gtg ggc gca ggc ggg    480
Gly Val Thr Ile Pro Thr Gly Ala Cys Pro Gly Val Gly Ala Gly Gly
145             150             155             160

cac atc ctc ggc ggg gga tac ggc ccg ctg tcg cgc cga ttc ggt tcg    528
His Ile Leu Gly Gly Gly Tyr Gly Pro Leu Ser Arg Arg Phe Gly Ser
                165             170             175

gtc gtc gac tac ctt caa ggc gtc gag gtc gtc gtg gtc gac cag gcc    576
Val Val Asp Tyr Leu Gln Gly Val Glu Val Val Val Val Asp Gln Ala
                180             185             190

ggt gaa gtg cac atc gtc gag gcc gac cgg aac tcc acg ggc gcc ggt    624
Gly Glu Val His Ile Val Glu Ala Asp Arg Asn Ser Thr Gly Ala Gly
            195             200             205

cac gac ttg tgg tgg gcg cac acc ggt ggc ggt ggc ggc aac ttc ggg    672
His Asp Leu Trp Trp Ala His Thr Gly Gly Gly Gly Gly Asn Phe Gly
            210             215             220

atc gtc acc agg ttt tgg ctc cga acg ccg gac gtg gtc agc acc gac    720
Ile Val Thr Arg Phe Trp Leu Arg Thr Pro Asp Val Val Ser Thr Asp
225             230             235             240

gcc gca gag ctc ctg cca cgg ccg ccc gcg aca gtg ctg ctc cga tcg    768
```

```
    Ala Ala Glu Leu Leu Pro Arg Pro Pro Ala Thr Val Leu Leu Arg Ser
                    245             250                 255


    ttc cac tgg ccg tgg cac gaa ctg aca gag cag tca ttc gcc gtg ctc    816
    Phe His Trp Pro Trp His Glu Leu Thr Glu Gln Ser Phe Ala Val Leu
                    260             265                 270


    cta cag aac ttc ggc aat tgg tac gag cag cac agc gcg cct gaa tcc    864
    Leu Gln Asn Phe Gly Asn Trp Tyr Glu Gln His Ser Ala Pro Glu Ser
                    275             280                 285


    acg caa ctc ggg ttg ttc agc acg ctc gtc tgc gca cac cgg caa gct    912
    Thr Gln Leu Gly Leu Phe Ser Thr Leu Val Cys Ala His Arg Gln Ala
                290             295                 300


    ggc tac gtc acg ctg aac gtt cac ctg gac ggc acg gat ccg aac gcg    960
    Gly Tyr Val Thr Leu Asn Val His Leu Asp Gly Thr Asp Pro Asn Ala
    305                 310                 315                 320


    gaa cgc acc ctg gcc gaa cac ctg tcg gcg atc aac gcc cag gtc ggc   1008
    Glu Arg Thr Leu Ala Glu His Leu Ser Ala Ile Asn Ala Gln Val Gly
                    325                 330                 335


    gtg act cca gcc gaa ggg ctg cgg gaa acc ctg ccg tgg ttg cga tcg   1056
    Val Thr Pro Ala Glu Gly Leu Arg Glu Thr Leu Pro Trp Leu Arg Ser
                340             345                 350


    acc cag gtg gcc ggg gcg atc gcc gaa ggc ggc gaa ccg ggc atg caa   1104
    Thr Gln Val Ala Gly Ala Ile Ala Glu Gly Gly Glu Pro Gly Met Gln
                355             360                 365


    cgg acc aag gtc aaa gcc gcc tac ttg cgc acc ggg ctg tcc gaa gct   1152
    Arg Thr Lys Val Lys Ala Ala Tyr Leu Arg Thr Gly Leu Ser Glu Ala
                370             375                 380


    caa cta gcc acg gtt tac cgg cgg ctg acc gtc tac gga tac gac aac   1200
    Gln Leu Ala Thr Val Tyr Arg Arg Leu Thr Val Tyr Gly Tyr Asp Asn
    385                 390                 395                 400


    cct gcg gcg gcg ctg ttg ctg ctc ggt tac ggc ggt atg gcg aat gcc   1248
    Pro Ala Ala Ala Leu Leu Leu Leu Gly Tyr Gly Gly Met Ala Asn Ala
                    405                 410                 415


    gtg gct ccg tcg gcc acc gca ctc gct cag cgc gac tcg gtt ctc aaa   1296
    Val Ala Pro Ser Ala Thr Ala Leu Ala Gln Arg Asp Ser Val Leu Lys
                420             425                 430


    gcg ctg ttc gtc acg aac tgg tcg gag ccc gcc gag gac gag cgg cat   1344
```

105

```
Ala Leu Phe Val Thr Asn Trp Ser Glu Pro Ala Glu Asp Glu Arg His
        435                 440                 445


ctg acc tgg att cgc ggt ttc tac cgc gag atg tac gcc gaa acc ggc    1392
Leu Thr Trp Ile Arg Gly Phe Tyr Arg Glu Met Tyr Ala Glu Thr Gly
        450                 455                 460


gga gtt ccg gtg cca ggt acc cgt gtc gac ggc tcc tac atc aac tac    1440
Gly Val Pro Val Pro Gly Thr Arg Val Asp Gly Ser Tyr Ile Asn Tyr
465                 470                 475                 480


ccg gac acc gac ttg gcc gat cca ttg tgg aac acc tcc ggt gtt gcc    1488
Pro Asp Thr Asp Leu Ala Asp Pro Leu Trp Asn Thr Ser Gly Val Ala
                485                 490                 495


tgg cac gac ctg tac tac aaa gac aac tac ccg cgg ctg cag cgg gcc    1536
Trp His Asp Leu Tyr Tyr Lys Asp Asn Tyr Pro Arg Leu Gln Arg Ala
                500                 505                 510


aaa gcg cgg tgg gat ccg cag aac atc ttc cag cac ggc ctg tcg atc    1584
Lys Ala Arg Trp Asp Pro Gln Asn Ile Phe Gln His Gly Leu Ser Ile
        515                 520                 525


aaa ccg ccg gca cgg ctt tca ccc ggt cag cca tga                    1620
Lys Pro Pro Ala Arg Leu Ser Pro Gly Gln Pro
        530                 535



<210> 16
<211> 539
<212> PRT
<213> Saccharopolyspora spinosa

<400> 16
Met Ile Ser Ala Ala Gly Glu Gln Ser Gly Pro Val Arg Lys Gly Gly
1                   5                   10                  15


Ala Val Pro Glu Phe His Asp Pro Ala Pro Met Asn Arg Arg Thr Pro
                20                  25                  30


Gly Thr Glu Ile Thr Val Glu Pro Asp Asp Pro Arg Tyr Pro Asp Leu
            35                  40                  45


Val Val Gly His Asn Pro Arg Phe Thr Gly Lys Pro Glu Arg Ile His
        50                  55                  60


Ile Ala Ser Ser Ala Glu Asp Val Val His Ala Val Ala Asp Ala Val
65                  70                  75                  80
```

```
Arg Thr Gly Arg Arg Val Gly Val Arg Ser Gly Gly His Cys Phe Glu
            85                  90                  95

Asn Leu Val Ala Asp Pro Ala Ile Arg Val Leu Val Asp Leu Ser Glu
            100                 105                 110

Leu Asn Arg Val Tyr Tyr Asp Ser Thr Arg Gly Ala Phe Ala Ile Glu
            115                 120                 125

Ala Gly Ala Ala Leu Gly Gln Val Tyr Arg Thr Leu Phe Lys Asn Trp
    130                 135                 140

Gly Val Thr Ile Pro Thr Gly Ala Cys Pro Gly Val Gly Ala Gly Gly
145                 150                 155                 160

His Ile Leu Gly Gly Gly Tyr Gly Pro Leu Ser Arg Arg Phe Gly Ser
                165                 170                 175

Val Val Asp Tyr Leu Gln Gly Val Glu Val Val Val Asp Gln Ala
                180                 185                 190

Gly Glu Val His Ile Val Glu Ala Asp Arg Asn Ser Thr Gly Ala Gly
    195                 200                 205

His Asp Leu Trp Trp Ala His Thr Gly Gly Gly Gly Gly Asn Phe Gly
    210                 215                 220

Ile Val Thr Arg Phe Trp Leu Arg Thr Pro Asp Val Val Ser Thr Asp
225                 230                 235                 240

Ala Ala Glu Leu Leu Pro Arg Pro Pro Ala Thr Val Leu Leu Arg Ser
                245                 250                 255

Phe His Trp Pro Trp His Glu Leu Thr Glu Gln Ser Phe Ala Val Leu
                260                 265                 270

Leu Gln Asn Phe Gly Asn Trp Tyr Glu Gln His Ser Ala Pro Glu Ser
                275                 280                 285

Thr Gln Leu Gly Leu Phe Ser Thr Leu Val Cys Ala His Arg Gln Ala
                290                 295                 300

Gly Tyr Val Thr Leu Asn Val His Leu Asp Gly Thr Asp Pro Asn Ala
305                 310                 315                 320

Glu Arg Thr Leu Ala Glu His Leu Ser Ala Ile Asn Ala Gln Val Gly
                325                 330                 335
```

107

```
Val Thr Pro Ala Glu Gly Leu Arg Glu Thr Leu Pro Trp Leu Arg Ser
        340             345              350

Thr Gln Val Ala Gly Ala Ile Ala Glu Gly Gly Glu Pro Gly Met Gln
        355             360              365

Arg Thr Lys Val Lys Ala Ala Tyr Leu Arg Thr Gly Leu Ser Glu Ala
    370             375             380

Gln Leu Ala Thr Val Tyr Arg Arg Leu Thr Val Tyr Gly Tyr Asp Asn
385             390             395             400

Pro Ala Ala Ala Leu Leu Leu Leu Gly Tyr Gly Gly Met Ala Asn Ala
            405             410             415

Val Ala Pro Ser Ala Thr Ala Leu Ala Gln Arg Asp Ser Val Leu Lys
        420             425             430

Ala Leu Phe Val Thr Asn Trp Ser Glu Pro Ala Glu Asp Glu Arg His
        435             440             445

Leu Thr Trp Ile Arg Gly Phe Tyr Arg Glu Met Tyr Ala Glu Thr Gly
    450             455             460

Gly Val Pro Val Pro Gly Thr Arg Val Asp Gly Ser Tyr Ile Asn Tyr
465             470             475             480

Pro Asp Thr Asp Leu Ala Asp Pro Leu Trp Asn Thr Ser Gly Val Ala
            485             490             495

Trp His Asp Leu Tyr Tyr Lys Asp Asn Tyr Pro Arg Leu Gln Arg Ala
        500             505             510

Lys Ala Arg Trp Asp Pro Gln Asn Ile Phe Gln His Gly Leu Ser Ile
        515             520             525

Lys Pro Pro Ala Arg Leu Ser Pro Gly Gln Pro
530             535
```

<210> 17
<211> 1194
<212> DNA
<213> Saccharopolyspora spinosa

<220>

<221> CDS
<222> (1)..(1191)
<223> ORF6; Methyltransferase

<400> 17
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atg tcc aca acg cac gag atc gaa acc gtg gaa cgc atc atc ctc gcc      48
Met Ser Thr Thr His Glu Ile Glu Thr Val Glu Arg Ile Ile Leu Ala
 1               5                  10                  15

gcc gga tcc agt gcg gcg agc ctg gcc gac ctg acc acc gaa ctc gga      96
Ala Gly Ser Ser Ala Ala Ser Leu Ala Asp Leu Thr Thr Glu Leu Gly
             20                  25                  30

ctc gcc agg atc gca ccc gtg ctg atc gac gag atc ctc ttc cgc gcg     144
Leu Ala Arg Ile Ala Pro Val Leu Ile Asp Glu Ile Leu Phe Arg Ala
         35                  40                  45

gaa ccg gcc ccc gac atc gaa cgg acc gag gtc gcg gtc cag atc acc     192
Glu Pro Ala Pro Asp Ile Glu Arg Thr Glu Val Ala Val Gln Ile Thr
     50                  55                  60

cac cga ggc gag acc gtt gac ttc gtc ctg acg cta cag tcc ggt gag     240
His Arg Gly Glu Thr Val Asp Phe Val Leu Thr Leu Gln Ser Gly Glu
 65                  70                  75                  80

ctg atc aag gcc gag caa cga ccg gtc gga gac gtc ccg ctg cgg atc     288
Leu Ile Lys Ala Glu Gln Arg Pro Val Gly Asp Val Pro Leu Arg Ile
                 85                  90                  95

ggt tac gag ctc acc gat ctc atc gcc gag ttg ttc ggc cca gga gct     336
Gly Tyr Glu Leu Thr Asp Leu Ile Ala Glu Leu Phe Gly Pro Gly Ala
                100                 105                 110

ccc agg gcc gtc ggc gcc cgg agc acc aac ttc ctc cga acc acc aca     384
Pro Arg Ala Val Gly Ala Arg Ser Thr Asn Phe Leu Arg Thr Thr Thr
            115                 120                 125

tcc ggt tcg ata ccc ggt ccg tcg gaa ctg tcc gat ggc ttc cag gcc     432
Ser Gly Ser Ile Pro Gly Pro Ser Glu Leu Ser Asp Gly Phe Gln Ala
        130                 135                 140

atc tcc gca gtg gtc gcc ggc tgc ggg cac cga cgt ccc gac ctc aac     480
Ile Ser Ala Val Val Ala Gly Cys Gly His Arg Arg Pro Asp Leu Asn
145                 150                 155                 160

ttg ctc gcc tcc cac tac cgc acg gac aag tgg ggc ggc ctg cac tgg     528
Leu Leu Ala Ser His Tyr Arg Thr Asp Lys Trp Gly Gly Leu His Trp
                165                 170                 175
```

```
ttc acc ccg cta tac gag cga cac ctc ggc gag ttc cgt gat cgc ccg    576
Phe Thr Pro Leu Tyr Glu Arg His Leu Gly Glu Phe Arg Asp Arg Pro
            180                 185                 190

gtg cgc atc ctg gag atc ggt gtc ggt ggc tac aac ttc gac ggt ggc    624
Val Arg Ile Leu Glu Ile Gly Val Gly Gly Tyr Asn Phe Asp Gly Gly
            195                 200                 205

ggc ggc gaa tcc ctg aag atg tgg aag cgc tac ttc cac cgc ggc ctc    672
Gly Gly Glu Ser Leu Lys Met Trp Lys Arg Tyr Phe His Arg Gly Leu
            210                 215                 220

gtg ttc ggg atg gac gtt ttc gac aag tcc ttc ctc gac cag cag agg    720
Val Phe Gly Met Asp Val Phe Asp Lys Ser Phe Leu Asp Gln Gln Arg
225                 230                 235                 240

ctc tgc acc gtc cgc gcc gac cag agc aag ccc gag gag ctg gcc gcc    768
Leu Cys Thr Val Arg Ala Asp Gln Ser Lys Pro Glu Glu Leu Ala Ala
                245                 250                 255

gtt gac gac aag tac gga ccg ttc gac atc atc atc gac gat ggc agc    816
Val Asp Asp Lys Tyr Gly Pro Phe Asp Ile Ile Ile Asp Asp Gly Ser
                260                 265                 270

cac atc aac gga cac gtg cgc aca tcc ctg gaa acg ctg ttc ccc cgg    864
His Ile Asn Gly His Val Arg Thr Ser Leu Glu Thr Leu Phe Pro Arg
            275                 280                 285

ttg cgc agc ggt ggc gta tac gtg atc gag gat ctg tgg acg acc tat    912
Leu Arg Ser Gly Gly Val Tyr Val Ile Glu Asp Leu Trp Thr Thr Tyr
            290                 295                 300

gct ccc gga ttc ggc ggg cag gcg cag tgc ccg gcc gca ccc ggc acc    960
Ala Pro Gly Phe Gly Gly Gln Ala Gln Cys Pro Ala Ala Pro Gly Thr
305                 310                 315                 320

acg gtc agc ctg ctc aag aac ctg ttg gaa ggc gtt cag cac gag gag   1008
Thr Val Ser Leu Leu Lys Asn Leu Leu Glu Gly Val Gln His Glu Glu
                325                 330                 335

cag ccg cat gcg ggc tcg tac gag ccg agc tac ctg gaa cgc aat ttg   1056
Gln Pro His Ala Gly Ser Tyr Glu Pro Ser Tyr Leu Glu Arg Asn Leu
                340                 345                 350

gtc ggc ctc cac acc tac cac aac atc gcg ttc ctg gag aaa ggc gtc   1104
Val Gly Leu His Thr Tyr His Asn Ile Ala Phe Leu Glu Lys Gly Val
            355                 360                 365
```

110

```
aac gcc gaa ggc ggc gtt cct gct tgg gtg cca agg agt ctg gac gac      1152
Asn Ala Glu Gly Gly Val Pro Ala Trp Val Pro Arg Ser Leu Asp Asp
        370             375             380

ata ttg cac ctg gcc gac gtg aac agc gcg gag gac gag tga            1194
Ile Leu His Leu Ala Asp Val Asn Ser Ala Glu Asp Glu
385             390             395
```

<210> 18
<211> 397
<212> PRT
<213> Saccharopolyspora spinosa

<400> 18

```
Met Ser Thr Thr His Glu Ile Glu Thr Val Glu Arg Ile Ile Leu Ala
 1               5                   10                  15

Ala Gly Ser Ser Ala Ala Ser Leu Ala Asp Leu Thr Thr Glu Leu Gly
            20                  25                  30

Leu Ala Arg Ile Ala Pro Val Leu Ile Asp Glu Ile Leu Phe Arg Ala
            35                  40                  45

Glu Pro Ala Pro Asp Ile Glu Arg Thr Glu Val Ala Val Gln Ile Thr
        50                  55                  60

His Arg Gly Glu Thr Val Asp Phe Val Leu Thr Leu Gln Ser Gly Glu
65                  70                  75                  80

Leu Ile Lys Ala Glu Gln Arg Pro Val Gly Asp Val Pro Leu Arg Ile
                85                  90                  95

Gly Tyr Glu Leu Thr Asp Leu Ile Ala Glu Leu Phe Gly Pro Gly Ala
            100                 105                 110

Pro Arg Ala Val Gly Ala Arg Ser Thr Asn Phe Leu Arg Thr Thr Thr
            115                 120                 125

Ser Gly Ser Ile Pro Gly Pro Ser Glu Leu Ser Asp Gly Phe Gln Ala
            130                 135                 140

Ile Ser Ala Val Val Ala Gly Cys Gly His Arg Arg Pro Asp Leu Asn
145                 150                 155                 160

Leu Leu Ala Ser His Tyr Arg Thr Asp Lys Trp Gly Gly Leu His Trp
                165                 170                 175
```

```
Phe Thr Pro Leu Tyr Glu Arg His Leu Gly Glu Phe Arg Asp Arg Pro
            180             185             190

Val Arg Ile Leu Glu Ile Gly Val Gly Gly Tyr Asn Phe Asp Gly Gly
            195             200             205

Gly Gly Glu Ser Leu Lys Met Trp Lys Arg Tyr Phe His Arg Gly Leu
        210             215             220

Val Phe Gly Met Asp Val Phe Asp Lys Ser Phe Leu Asp Gln Gln Arg
225             230             235             240

Leu Cys Thr Val Arg Ala Asp Gln Ser Lys Pro Glu Glu Leu Ala Ala
                245             250             255

Val Asp Asp Lys Tyr Gly Pro Phe Asp Ile Ile Ile Asp Asp Gly Ser
            260             265             270

His Ile Asn Gly His Val Arg Thr Ser Leu Glu Thr Leu Phe Pro Arg
            275             280             285

Leu Arg Ser Gly Gly Val Tyr Val Ile Glu Asp Leu Trp Thr Thr Tyr
            290             295             300

Ala Pro Gly Phe Gly Gly Gln Ala Gln Cys Pro Ala Ala Pro Gly Thr
305             310             315             320

Thr Val Ser Leu Leu Lys Asn Leu Leu Glu Gly Val Gln His Glu Glu
                325             330             335

Gln Pro His Ala Gly Ser Tyr Glu Pro Ser Tyr Leu Glu Arg Asn Leu
            340             345             350

Val Gly Leu His Thr Tyr His Asn Ile Ala Phe Leu Glu Lys Gly Val
            355             360             365

Asn Ala Glu Gly Gly Val Pro Ala Trp Val Pro Arg Ser Leu Asp Asp
    370             375             380

Ile Leu His Leu Ala Asp Val Asn Ser Ala Glu Asp Glu
385             390             395
```

<210> 19
<211> 900
<212> DNA

<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(897)
<223> ORF7; O-Methyltransferase

<400> 19
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gtg aac agc aga ggg gcg aac aca cag gca ttt ccg acc gcg gat cag    48
Val Asn Ser Arg Gly Ala Asn Thr Gln Ala Phe Pro Thr Ala Asp Gln
 1               5                  10                  15

gtg gag tcc atc ttc gat gcg ttg gcg cac ggg cgt ccc ctg cac cac    96
Val Glu Ser Ile Phe Asp Ala Leu Ala His Gly Arg Pro Leu His His
             20                  25                  30

ggt tac tgg gcg ggc ggg tat cgg gag gat gcc ggt gcc aca ccg tgg   144
Gly Tyr Trp Ala Gly Gly Tyr Arg Glu Asp Ala Gly Ala Thr Pro Trp
         35                  40                  45

tcg gat gct gcc gac caa ctg acc gac ctg ttc atc gac aag gcc gcg   192
Ser Asp Ala Ala Asp Gln Leu Thr Asp Leu Phe Ile Asp Lys Ala Ala
     50                  55                  60

ctc cgt ccc gga gcg cac ctg ttc gac ctg ggc tgc ggc aat ggg cag   240
Leu Arg Pro Gly Ala His Leu Phe Asp Leu Gly Cys Gly Asn Gly Gln
 65                  70                  75                  80

ccc gta gtc cgt gcg gca tgc gcc agc ggc gtt cga gtc acc gga atc   288
Pro Val Val Arg Ala Ala Cys Ala Ser Gly Val Arg Val Thr Gly Ile
                 85                  90                  95

acc gtg aac gcc cag cat ctc gcc gcc gcc acc agg ctc gcc aac gag   336
Thr Val Asn Ala Gln His Leu Ala Ala Ala Thr Arg Leu Ala Asn Glu
                100                 105                 110

acc gga ctg gcc ggc agt ctt gag ttc gat cta gtc gac ggc gcc cag   384
Thr Gly Leu Ala Gly Ser Leu Glu Phe Asp Leu Val Asp Gly Ala Gln
         115                 120                 125

ctg ccc tac ccg gac ggt ttc ttt cag gcc gca tgg gcg atg cag tcc   432
Leu Pro Tyr Pro Asp Gly Phe Phe Gln Ala Ala Trp Ala Met Gln Ser
     130                 135                 140

gtc gtg cag atc gtg gac cag gcc gcc gcg atc cgc gag gtc cac cga   480
Val Val Gln Ile Val Asp Gln Ala Ala Ala Ile Arg Glu Val His Arg
145                 150                 155                 160
```

```
atc ctg gaa ccc ggc ggc cgg ttc gtc ctc gga gac atc atc act cgg    528
Ile Leu Glu Pro Gly Gly Arg Phe Val Leu Gly Asp Ile Ile Thr Arg
              165             170             175

gtt cga ctc ccg gaa gag tac gcg gcg gtt tgg acg ggc acg acc gcc    576
Val Arg Leu Pro Glu Glu Tyr Ala Ala Val Trp Thr Gly Thr Thr Ala
              180             185             190

cat acc ttg aac agc ttc acg gcg ctg gtc agc gaa gcc ggg ttc gag    624
His Thr Leu Asn Ser Phe Thr Ala Leu Val Ser Glu Ala Gly Phe Glu
              195             200             205

att ctc gaa gtc acc gac ctc acg gca cag acc agg tgc atg gtc tcc    672
Ile Leu Glu Val Thr Asp Leu Thr Ala Gln Thr Arg Cys Met Val Ser
          210             215             220

tgg tac gtc gac gag ttg ctc cgg aaa ctc gat gag ctc gcc ggc gtc    720
Trp Tyr Val Asp Glu Leu Leu Arg Lys Leu Asp Glu Leu Ala Gly Val
225             230             235             240

gag cct gcg gct gtc ggc acc tac cag caa cgc tac ttg gga gac atc    768
Glu Pro Ala Ala Val Gly Thr Tyr Gln Gln Arg Tyr Leu Gly Asp Ile
              245             250             255

gcg gcg aag cac gga ccg gga cca gca cag ctg atc gcc gcg gtt gcg    816
Ala Ala Lys His Gly Pro Gly Pro Ala Gln Leu Ile Ala Ala Val Ala
              260             265             270

gaa tac cgg aaa cat ccg gat tac gcc aga aac gag gaa agc atg ggt    864
Glu Tyr Arg Lys His Pro Asp Tyr Ala Arg Asn Glu Glu Ser Met Gly
              275             280             285

ttc atg ctc ctg cag gct cga aag aag cag tcc tga                    900
Phe Met Leu Leu Gln Ala Arg Lys Lys Gln Ser
              290             295
```

```
<210> 20
<211> 299
<212> PRT
<213> Saccharopolyspora spinosa

<400> 20
Val Asn Ser Arg Gly Ala Asn Thr Gln Ala Phe Pro Thr Ala Asp Gln
1               5               10              15

Val Glu Ser Ile Phe Asp Ala Leu Ala His Gly Arg Pro Leu His His
              20              25              30
```

Gly Tyr Trp Ala Gly Gly Tyr Arg Glu Asp Ala Gly Ala Thr Pro Trp
        35   40   45

Ser Asp Ala Ala Asp Gln Leu Thr Asp Leu Phe Ile Asp Lys Ala Ala
    50   55   60

Leu Arg Pro Gly Ala His Leu Phe Asp Leu Gly Cys Gly Asn Gly Gln
65   70   75   80

Pro Val Val Arg Ala Ala Cys Ala Ser Gly Val Arg Val Thr Gly Ile
            85   90   95

Thr Val Asn Ala Gln His Leu Ala Ala Ala Thr Arg Leu Ala Asn Glu
            100   105   110

Thr Gly Leu Ala Gly Ser Leu Glu Phe Asp Leu Val Asp Gly Ala Gln
        115   120   125

Leu Pro Tyr Pro Asp Gly Phe Phe Gln Ala Ala Trp Ala Met Gln Ser
    130   135   140

Val Val Gln Ile Val Asp Gln Ala Ala Ala Ile Arg Glu Val His Arg
145   150   155   160

Ile Leu Glu Pro Gly Gly Arg Phe Val Leu Gly Asp Ile Ile Thr Arg
            165   170   175

Val Arg Leu Pro Glu Glu Tyr Ala Ala Val Trp Thr Gly Thr Thr Ala
        180   185   190

His Thr Leu Asn Ser Phe Thr Ala Leu Val Ser Glu Ala Gly Phe Glu
    195   200   205

Ile Leu Glu Val Thr Asp Leu Thr Ala Gln Thr Arg Cys Met Val Ser
    210   215   220

Trp Tyr Val Asp Glu Leu Leu Arg Lys Leu Asp Glu Leu Ala Gly Val
225   230   235   240

Glu Pro Ala Ala Val Gly Thr Tyr Gln Gln Arg Tyr Leu Gly Asp Ile
            245   250   255

Ala Ala Lys His Gly Pro Gly Pro Ala Gln Leu Ile Ala Ala Val Ala
            260   265   270

Glu Tyr Arg Lys His Pro Asp Tyr Ala Arg Asn Glu Glu Ser Met Gly
    275   280   285

115

```
           Phe Met Leu Leu Gln Ala Arg Lys Lys Gln Ser
               290             295
```

```
<210> 21
<211> 1167
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(1164)
<223> ORF8; Cyclisierungsenzym

<400> 21
atg gcc tcc gag cac gcc agc ctg gtc ggc gac gat ctg cgg gca ccc      48
Met Ala Ser Glu His Ala Ser Leu Val Gly Asp Asp Leu Arg Ala Pro
 1               5                  10                  15

gcg gat gat ccc ttc tac cga ccg ccg acg ccg cta ccg ccg ggt gtc      96
Ala Asp Asp Pro Phe Tyr Arg Pro Pro Thr Pro Leu Pro Pro Gly Val
               20                  25                  30

ccg ggc acg ctc ctc agg gcc cgg ccc gtc tcg gca ctg cgc ggc acg     144
Pro Gly Thr Leu Leu Arg Ala Arg Pro Val Ser Ala Leu Arg Gly Thr
           35                  40                  45

ggc gaa ccc gtc gca gcc aag gcc tgg caa atc ctc tac cgg tcc aac     192
Gly Glu Pro Val Ala Ala Lys Ala Trp Gln Ile Leu Tyr Arg Ser Asn
       50                  55                  60

tcc gcc ctt ggc atg ccg aac gcc gtc tcc ggc acc gtt ctg gtg ccg     240
Ser Ala Leu Gly Met Pro Asn Ala Val Ser Gly Thr Val Leu Val Pro
 65                  70                  75                  80

aac atc ccg tgg ccg cgc gaa gat cgc ccc atc atc act ttc gca gtg     288
Asn Ile Pro Trp Pro Arg Glu Asp Arg Pro Ile Ile Thr Phe Ala Val
                   85                  90                  95

ggc acc cac ggc ctc ggt agc caa gtt gcc ccg tcg tac ctg ctt cga     336
Gly Thr His Gly Leu Gly Ser Gln Val Ala Pro Ser Tyr Leu Leu Arg
               100                 105                 110

acc gga acc gag ccg gag acc gag ctg atc gcc gtg gcc ctc gac cgc     384
Thr Gly Thr Glu Pro Glu Thr Glu Leu Ile Ala Val Ala Leu Asp Arg
           115                 120                 125
```

116

```
ggg tgg gcc gtg gtc atc acc gac tac gaa ggc ctc ggt act cct gga    432
Gly Trp Ala Val Val Ile Thr Asp Tyr Glu Gly Leu Gly Thr Pro Gly
    130                     135                 140

acc cac acc tac acc gtc ggc agg gcg cag gga cac gcc atg ctc gat    480
Thr His Thr Tyr Thr Val Gly Arg Ala Gln Gly His Ala Met Leu Asp
145                     150                 155                 160

gcc gcc cgc gct gcg caa cgg cta ccg ggc tcc ggc ctg acg acc gac    528
Ala Ala Arg Ala Ala Gln Arg Leu Pro Gly Ser Gly Leu Thr Thr Asp
                    165                 170                 175

tgc ccg gtc ggc atc tgg ggc tat gcg cag ggt ggg caa gcg tcg gcc    576
Cys Pro Val Gly Ile Trp Gly Tyr Ala Gln Gly Gly Gln Ala Ser Ala
                180                 185                 190

ttc gcc ggc gaa ctg cac ccc acc tac gca cct gaa ctg cga atc cgc    624
Phe Ala Gly Glu Leu His Pro Thr Tyr Ala Pro Glu Leu Arg Ile Arg
            195                 200                 205

gct gcg gcc gca ggt gcg gtg ccg atc gat ctg ctg gac atc atc cac    672
Ala Ala Ala Ala Gly Ala Val Pro Ile Asp Leu Leu Asp Ile Ile His
    210                 215                 220

cga aat gac ggg gtg ttc acc ggg ccg gtg ctg gcc ggc ctg gtc ggg    720
Arg Asn Asp Gly Val Phe Thr Gly Pro Val Leu Ala Gly Leu Val Gly
225                 230                 235                 240

cat gcc gct gcc tac ccc gat ctg cca ttc gac gag ctt ctc acc gaa    768
His Ala Ala Ala Tyr Pro Asp Leu Pro Phe Asp Glu Leu Leu Thr Glu
                245                 250                 255

gcg ggt cgt acc gcc gtt gat caa gtg cgc gag ctc ggt gca ccg gag    816
Ala Gly Arg Thr Ala Val Asp Gln Val Arg Glu Leu Gly Ala Pro Glu
            260                 265                 270

ctc gtc acc cgc ttc ctc ggc cgc gag ctg agc gac ttc ctc gac act    864
Leu Val Thr Arg Phe Leu Gly Arg Glu Leu Ser Asp Phe Leu Asp Thr
            275                 280                 285

tcc ggc ctt ttc gag caa cct cga tgg cgc gca cga ctg gcc gaa agc    912
Ser Gly Leu Phe Glu Gln Pro Arg Trp Arg Ala Arg Leu Ala Glu Ser
    290                 295                 300

gtc gca ggt agg aac ggt ggc ccg gtg gtc ccc acg ctc gtc tac cac    960
Val Ala Gly Arg Asn Gly Gly Pro Val Val Pro Thr Leu Val Tyr His
305                 310                 315                 320
```

117

```
agc acg gac gac gag atc gtt ccg ttc gca ttc ggc gag cga ctc cgg    1008
Ser Thr Asp Asp Glu Ile Val Pro Phe Ala Phe Gly Glu Arg Leu Arg
                325             330             335


gac agc tac cgc gcg gcg ggt acg cca gtg cgg tgg cat ccg ctc tcc    1056
Asp Ser Tyr Arg Ala Ala Gly Thr Pro Val Arg Trp His Pro Leu Ser
                340             345             350


gga ttg gct cac ttt ccc gcc gcc ctg gcc agc tcg cga gtg gtc gtc    1104
Gly Leu Ala His Phe Pro Ala Ala Leu Ala Ser Ser Arg Val Val Val
                355             360             365


tcg tgg ttc gac gag cac ttc tcc gag ccg tcc gcg atc agc ggt ccg    1152
Ser Trp Phe Asp Glu His Phe Ser Glu Pro Ser Ala Ile Ser Gly Pro
          370             375             380


cga gat gcc agg tga                                                 1167
Arg Asp Ala Arg
385
```

<210> 22
<211> 388
<212> PRT
<213> Saccharopolyspora spinosa

<400> 22

```
Met Ala Ser Glu His Ala Ser Leu Val Gly Asp Asp Leu Arg Ala Pro
1               5               10              15


Ala Asp Asp Pro Phe Tyr Arg Pro Pro Thr Pro Leu Pro Pro Gly Val
                20              25              30


Pro Gly Thr Leu Leu Arg Ala Arg Pro Val Ser Ala Leu Arg Gly Thr
          35              40              45


Gly Glu Pro Val Ala Ala Lys Ala Trp Gln Ile Leu Tyr Arg Ser Asn
    50              55              60


Ser Ala Leu Gly Met Pro Asn Ala Val Ser Gly Thr Val Leu Val Pro
65              70              75              80


Asn Ile Pro Trp Pro Arg Glu Asp Arg Pro Ile Ile Thr Phe Ala Val
                85              90              95


Gly Thr His Gly Leu Gly Ser Gln Val Ala Pro Ser Tyr Leu Leu Arg
          100             105             110
```

```
Thr Gly Thr Glu Pro Glu Thr Glu Leu Ile Ala Val Ala Leu Asp Arg
        115             120             125

Gly Trp Ala Val Val Ile Thr Asp Tyr Glu Gly Leu Gly Thr Pro Gly
        130             135             140

Thr His Thr Tyr Thr Val Gly Arg Ala Gln Gly His Ala Met Leu Asp
145             150             155             160

Ala Ala Arg Ala Ala Gln Arg Leu Pro Gly Ser Gly Leu Thr Thr Asp
                165             170             175

Cys Pro Val Gly Ile Trp Gly Tyr Ala Gln Gly Gly Gln Ala Ser Ala
            180             185             190

Phe Ala Gly Glu Leu His Pro Thr Tyr Ala Pro Glu Leu Arg Ile Arg
        195             200             205

Ala Ala Ala Ala Gly Ala Val Pro Ile Asp Leu Leu Asp Ile Ile His
    210             215             220

Arg Asn Asp Gly Val Phe Thr Gly Pro Val Leu Ala Gly Leu Val Gly
225             230             235             240

His Ala Ala Ala Tyr Pro Asp Leu Pro Phe Asp Glu Leu Leu Thr Glu
                245             250             255

Ala Gly Arg Thr Ala Val Asp Gln Val Arg Glu Leu Gly Ala Pro Glu
            260             265             270

Leu Val Thr Arg Phe Leu Gly Arg Glu Leu Ser Asp Phe Leu Asp Thr
            275             280             285

Ser Gly Leu Phe Glu Gln Pro Arg Trp Arg Ala Arg Leu Ala Glu Ser
    290             295                 300

Val Ala Gly Arg Asn Gly Gly Pro Val Val Pro Thr Leu Val Tyr His
305                 310             315             320

Ser Thr Asp Asp Glu Ile Val Pro Phe Ala Phe Gly Glu Arg Leu Arg
                325             330             335

Asp Ser Tyr Arg Ala Ala Gly Thr Pro Val Arg Trp His Pro Leu Ser
            340             345             350

Gly Leu Ala His Phe Pro Ala Ala Leu Ala Ser Ser Arg Val Val Val
            355             360             365
```

```
Ser Trp Phe Asp Glu His Phe Ser Glu Pro Ser Ala Ile Ser Gly Pro
    370                 375                 380

Arg Asp Ala Arg    · .
385
```

```
<210> 23
<211> 1011
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(1008)
<223> ORF9; 2,3-Reduktase

<400> 23
atg acc agc tcg atg cga aag ccg gtg cgc atc ggt gtg ctc ggg tgc    48
Met Thr Ser Ser Met Arg Lys Pro Val Arg Ile Gly Val Leu Gly Cys
  1               5                  10                  15

gct tcc ttc gcg tgg cga cgg atg ctg ccc gcg atg tgc gac gtg gcc    96
Ala Ser Phe Ala Trp Arg Arg Met Leu Pro Ala Met Cys Asp Val Ala
             20                  25                  30

gaa aca gag gtg gtg gcg gtg gcg agc cgt gat ccg gcg aaa gcc gaa   144
Glu Thr Glu Val Val Ala Val Ala Ser Arg Asp Pro Ala Lys Ala Glu
         35                  40                  45

cgg ttc gca gcg cga ttc gaa tgc gag gcg gtg ctg ggt tac cag cgg   192
Arg Phe Ala Ala Arg Phe Glu Cys Glu Ala Val Leu Gly Tyr Gln Arg
     50                  55                  60

ctc ctg gag cgg ccg gac atc gat gcc gtc tac gtg ccg ttg ccg cct   240
Leu Leu Glu Arg Pro Asp Ile Asp Ala Val Tyr Val Pro Leu Pro Pro
 65                  70                  75                  80

ggc atg cat gca gag tgg atc ggc aag gcg ctt gag gca gac aaa cac   288
Gly Met His Ala Glu Trp Ile Gly Lys Ala Leu Glu Ala Asp Lys His
                 85                  90                  95

gtg ctt gcg gag aaa ccg ctg acg acg acg gcg tcc gac acc gct cgc   336
Val Leu Ala Glu Lys Pro Leu Thr Thr Thr Ala Ser Asp Thr Ala Arg
            100                 105                 110
```

120

```
ctg gtc ggg ctg gcc agg agg aag aac ctg ctg ctg cgg gag aat tac     384
Leu Val Gly Leu Ala Arg Arg Lys Asn Leu Leu Leu Arg Glu Asn Tyr
        115                 120                 125


ctg ttc ctc cac cac ggc cgg cac gac gtg gtc cgc gac ctg ctg caa     432
Leu Phe Leu His His Gly Arg His Asp Val Val Arg Asp Leu Leu Gln
        130                 135                 140


tcc ggg gag atc ggt gag ctc cgg gag ttc acc gcc gtg ttc gga att     480
Ser Gly Glu Ile Gly Glu Leu Arg Glu Phe Thr Ala Val Phe Gly Ile
145                 150                 155                 160


ccg ccg ctt ccc gac acg gac atc cgc tat cgc acc gaa ctc ggt ggc     528
Pro Pro Leu Pro Asp Thr Asp Ile Arg Tyr Arg Thr Glu Leu Gly Gly
                165                 170                 175


gga gcg ttg ctg gac atc ggt gtc tat ccc gcc cgt gcc gct cgg cac     576
Gly Ala Leu Leu Asp Ile Gly Val Tyr Pro Ala Arg Ala Ala Arg His
            180                 185                 190


ttt ctc ctc ggt ccg ctc acg gtt ctc ggc gca agc tcg cac gag gcc     624
Phe Leu Leu Gly Pro Leu Thr Val Leu Gly Ala Ser Ser His Glu Ala
        195                 200                 205


cag gag tcg ggc gtc gac ttg tcg ggc agc gtg ctg ctc caa tcg gaa     672
Gln Glu Ser Gly Val Asp Leu Ser Gly Ser Val Leu Leu Gln Ser Glu
        210                 215                 220


ggt ggc acc gtt gcc cac ctc gga tac ggt ttc gtg cac cac tac cgc     720
Gly Gly Thr Val Ala His Leu Gly Tyr Gly Phe Val His His Tyr Arg
225                 230                 235                 240


agc gcg tac gag ctg tgg ggg agt cgt ggg cga atc gtc gtc gac cgg     768
Ser Ala Tyr Glu Leu Trp Gly Ser Arg Gly Arg Ile Val Val Asp Arg
                245                 250                 255


gcg ttc acg ccg ccc gcc gag tgg cag gcc gtg atc cga atc gag cgg     816
Ala Phe Thr Pro Pro Ala Glu Trp Gln Ala Val Ile Arg Ile Glu Arg
                260                 265                 270


aag ggc gtt gtc gac gag ttg tcc ttg cca gcg gaa gat cag gtt cgc     864
Lys Gly Val Val Asp Glu Leu Ser Leu Pro Ala Glu Asp Gln Val Arg
            275                 280                 285


aag gcg gtc acc gcc ttc gca cgc gac atc aga gca ggg aca ggc gtg     912
Lys Ala Val Thr Ala Phe Ala Arg Asp Ile Arg Ala Gly Thr Gly Val
        290                 295                 300
```

```
gac gac cct gcg gtg gcc gga gat tcg ggc gaa tcg atg atc cag cag    960
Asp Asp Pro Ala Val Ala Gly Asp Ser Gly Glu Ser Met Ile Gln Gln
305             310             315             320


gcc gcg ctg gtg gag gcg atc ggt cag gcc cgt cgg tgc ggg tcc aca   1008
Ala Ala Leu Val Glu Ala Ile Gly Gln Ala Arg Arg Cys Gly Ser Thr
            325             330             335


tag                                                                1011
```

```
<210> 24
<211> 336
<212> PRT
<213> Saccharopolyspora spinosa

<400> 24
Met Thr Ser Ser Met Arg Lys Pro Val Arg Ile Gly Val Leu Gly Cys
1               5               10              15

Ala Ser Phe Ala Trp Arg Arg Met Leu Pro Ala Met Cys Asp Val Ala
            20              25              30

Glu Thr Glu Val Val Ala Val Ala Ser Arg Asp Pro Ala Lys Ala Glu
        35              40              45

Arg Phe Ala Ala Arg Phe Glu Cys Glu Ala Val Leu Gly Tyr Gln Arg
    50              55              60

Leu Leu Glu Arg Pro Asp Ile Asp Ala Val Tyr Val Pro Leu Pro Pro
65              70              75              80

Gly Met His Ala Glu Trp Ile Gly Lys Ala Leu Glu Ala Asp Lys His
            85              90              95

Val Leu Ala Glu Lys Pro Leu Thr Thr Thr Ala Ser Asp Thr Ala Arg
            100             105             110

Leu Val Gly Leu Ala Arg Arg Lys Asn Leu Leu Leu Arg Glu Asn Tyr
            115             120             125

Leu Phe Leu His His Gly Arg His Asp Val Val Arg Asp Leu Leu Gln
    130             135             140

Ser Gly Glu Ile Gly Glu Leu Arg Glu Phe Thr Ala Val Phe Gly Ile
145             150             155             160

Pro Pro Leu Pro Asp Thr Asp Ile Arg Tyr Arg Thr Glu Leu Gly Gly
```

                    165   170   175

Gly Ala Leu Leu Asp Ile Gly Val Tyr Pro Ala Arg Ala Ala Arg His
            180   185   190

Phe Leu Leu Gly Pro Leu Thr Val Leu Gly Ala Ser Ser His Glu Ala
        195   200   205

Gln Glu Ser Gly Val Asp Leu Ser Gly Ser Val Leu Leu Gln Ser Glu
        210   215   220

Gly Gly Thr Val Ala His Leu Gly Tyr Gly Phe Val His His Tyr Arg
225   230   235   240

Ser Ala Tyr Glu Leu Trp Gly Ser Arg Gly Arg Ile Val Val Asp Arg
            245   250   255

Ala Phe Thr Pro Pro Ala Glu Trp Gln Ala Val Ile Arg Ile Glu Arg
            260   265   270

Lys Gly Val Val Asp Glu Leu Ser Leu Pro Ala Glu Asp Gln Val Arg
        275   280   285

Lys Ala Val Thr Ala Phe Ala Arg Asp Ile Arg Ala Gly Thr Gly Val
        290   295   300

Asp Asp Pro Ala Val Ala Gly Asp Ser Gly Glu Ser Met Ile Gln Gln
305   310   315   320

Ala Ala Leu Val Glu Ala Ile Gly Gln Ala Arg Arg Cys Gly Ser Thr
            325   330   335

<210> 25
<211> 1461
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(1458)
<223> ORF10; 2,3-Dehydratase

<400> 25
atg agc agt tct gtc gaa gct gag gca agt gct gct gcg ccg ctc ggc   48
Met Ser Ser Ser Val Glu Ala Glu Ala Ser Ala Ala Ala Pro Leu Gly
  1   5   10   15

```
agc aac aac acg cgg cgg ttc gtc gac tct gcg ctg agc gct tgc aat    96
Ser Asn Asn Thr Arg Arg Phe Val Asp Ser Ala Leu Ser Ala Cys Asn
            20                  25                  30

ggc atg att ccg acc acg gag ttc cac tgc tgg ctc gcc gat cgg ctg   144
Gly Met Ile Pro Thr Thr Glu Phe His Cys Trp Leu Ala Asp Arg Leu
            35                  40                 ·45

ggc gag aac agc ttc gag acc aat cgc atc ccg ttc gac cgc ctg tcg   192
Gly Glu Asn Ser Phe Glu Thr Asn Arg Ile Pro Phe Asp Arg Leu Ser
        50                  55                  60

aaa tgg aaa ttc gat gcc agc acg gag aac ctg gtt cat gcc gac ggt   240
Lys Trp Lys Phe Asp Ala Ser Thr Glu Asn Leu Val His Ala Asp Gly
    65                  70                  75                  80

agg ttc ttc acg gta gaa ggc ctg cag gtc gag acc aac tat ggc gcg   288
Arg Phe Phe Thr Val Glu Gly Leu Gln Val Glu Thr Asn Tyr Gly Ala
                85                  90                  95

gca ccc agc tgg cac cag ccg atc atc aac cag gct gaa gta ggt atc   336
Ala Pro Ser Trp His Gln Pro Ile Ile Asn Gln Ala Glu Val Gly Ile
            100                 105                 110

ctc ggc att ctc gtc aag gag atc gac ggc gtg ctg cac tgc ctc atg   384
Leu Gly Ile Leu Val Lys Glu Ile Asp Gly Val Leu His Cys Leu Met
            115                 120                 125

tca gca aag atg gaa ccg ggc aac gtc aac gtc ctg cag ctc tcg ccg   432
Ser Ala Lys Met Glu Pro Gly Asn Val Asn Val Leu Gln Leu Ser Pro
        130                 135                 140

acg gtt cag gca act cgg agc aac tac acg cag gca cac cgt ggc agc   480
Thr Val Gln Ala Thr Arg Ser Asn Tyr Thr Gln Ala His Arg Gly Ser
145                 150                 155                 160

gtt ccg ccc tat gtg gac tac ttc ctc ggg cgg ggc cgc ggc cgc gtg   528
Val Pro Pro Tyr Val Asp Tyr Phe Leu Gly Arg Gly Arg Gly Arg Val
            165                 170                 175

ctg gta gac gtg ctc cag tct gaa cag ggg tcc tgg ttc tac cgg aag   576
Leu Val Asp Val Leu Gln Ser Glu Gln Gly Ser Trp Phe Tyr Arg Lys
            180                 185                 190

cgc aac cgg aac atg gtg gtg gaa gtc cag gag gaa gtg cca gtc ctg   624
Arg Asn Arg Asn Met Val Val Glu Val Gln Glu Glu Val Pro Val Leu
            195                 200                 205
```

124

```
cca gac ttc tgc tgg ttg acg ctc ggc cag gtg ctg gct ctc ctt cgt    672
Pro Asp Phe Cys Trp Leu Thr Leu Gly Gln Val Leu Ala Leu Leu Arg
    210             215                 220

cag gac aac atc gtc aac atg gac acc cgg acg gtg ctg tct tgc atc    720
Gln Asp Asn Ile Val Asn Met Asp Thr Arg Thr Val Leu Ser Cys Ile
225             230                 235                 240

ccg ttc cac gat tcc gcc acc gga ccc gaa cta gcc gcc tcg gag gag    768
Pro Phe His Asp Ser Ala Thr Gly Pro Glu Leu Ala Ala Ser Glu Glu
            245                 250                 255

ccc ttc cga cag gcg gtg gcc agg tcg ctc tcg cac ggc atc gat tcg    816
Pro Phe Arg Gln Ala Val Ala Arg Ser Leu Ser His Gly Ile Asp Ser
        260                 265                 270

tcg agt atc tcc gag gcg gtc ggt tgg ttc gag gaa gcc aag gcc cgc    864
Ser Ser Ile Ser Glu Ala Val Gly Trp Phe Glu Glu Ala Lys Ala Arg
        275                 280                 285

tac cgc ttg cgg gca acg cgc gtt ccg ctg agc agg gtc gac aag tgg    912
Tyr Arg Leu Arg Ala Thr Arg Val Pro Leu Ser Arg Val Asp Lys Trp
    290                 295                 300

tat cgc acc gat acc gag atc gcc cac cag gac ggc aag tac ttc gcg    960
Tyr Arg Thr Asp Thr Glu Ile Ala His Gln Asp Gly Lys Tyr Phe Ala
305                 310                 315                 320

gtg atc gcg gtg tcg gtg tcc gcg acc aat cgt gag gtc gcc agc tgg   1008
Val Ile Ala Val Ser Val Ser Ala Thr Asn Arg Glu Val Ala Ser Trp
                325                 330                 335

acg cag ccg atg atc gaa ccg cga gaa caa ggt gag atc gca ctg ttg   1056
Thr Gln Pro Met Ile Glu Pro Arg Glu Gln Gly Glu Ile Ala Leu Leu
            340                 345                 350

gtc aag cgg atc ggc gga gtg ctg cac ggt ttg gtc cac gct cgg gtg   1104
Val Lys Arg Ile Gly Gly Val Leu His Gly Leu Val His Ala Arg Val
        355                 360                 365

gag gct ggg tat aag tgg act gcg gaa atc gct ccc acg gtc cag tgc   1152
Glu Ala Gly Tyr Lys Trp Thr Ala Glu Ile Ala Pro Thr Val Gln Cys
        370                 375                 380

agt gtg gcc aac tac caa agc acc ccg tcg aac gac tgg ccg ccg ttc   1200
Ser Val Ala Asn Tyr Gln Ser Thr Pro Ser Asn Asp Trp Pro Pro Phe
385                 390                 395                 400
```

```
ttg gac gac gtg ctc acc gcc gat ccc gaa acc gtg cgg tac gaa tcg    1248
Leu Asp Asp Val Leu Thr Ala Asp Pro Glu Thr Val Arg Tyr Glu Ser
            405               410               415

atc ctg tcc gaa gaa ggc ggt cgg ttc tac cag gcg cag aac agg tac    1296
Ile Leu Ser Glu Glu Gly Gly Arg Phe Tyr Gln Ala Gln Asn Arg Tyr
            420               425               430

cgg atc atc gag gtg cat gag gac ttc gcg gca cga cct ccc agc gac    1344
Arg Ile Ile Glu Val His Glu Asp Phe Ala Ala Arg Pro Pro Ser Asp
            435               440               445

ttc cgg tgg atg act ttg gga cag ttg ggc gag ctg ctc cgg agc acc    1392
Phe Arg Trp Met Thr Leu Gly Gln Leu Gly Glu Leu Leu Arg Ser Thr
            450               455               460

cac ttc ttg aac atc cag gcg cgc agc ttg gtc gcc tcc ctg cat agc    1440
His Phe Leu Asn Ile Gln Ala Arg Ser Leu Val Ala Ser Leu His Ser
465               470               475               480

ttg tgg gcg ttg ggg cga tga                                        1461
Leu Trp Ala Leu Gly Arg
            485


<210> 26
<211> 486
<212> PRT
<213> Saccharopolyspora spinosa

<400> 26
Met Ser Ser Ser Val Glu Ala Glu Ala Ser Ala Ala Ala Pro Leu Gly
1               5               10               15

Ser Asn Asn Thr Arg Arg Phe Val Asp Ser Ala Leu Ser Ala Cys Asn
            20               25               30

Gly Met Ile Pro Thr Thr Glu Phe His Cys Trp Leu Ala Asp Arg Leu
            35               40               45

Gly Glu Asn Ser Phe Glu Thr Asn Arg Ile Pro Phe Asp Arg Leu Ser
            50               55               60

Lys Trp Lys Phe Asp Ala Ser Thr Glu Asn Leu Val His Ala Asp Gly
65               70               75               80

Arg Phe Phe Thr Val Glu Gly Leu Gln Val Glu Thr Asn Tyr Gly Ala
```

126

```
                        85                    90                    95

   Ala Pro Ser Trp His Gln Pro Ile Ile Asn Gln Ala Glu Val Gly Ile
               100                   105                   110

   Leu Gly Ile Leu Val Lys Glu Ile Asp Gly Val Leu His Cys Leu Met
               115                   120                   125

   Ser Ala Lys Met Glu Pro Gly Asn Val Asn Val Leu Gln Leu Ser Pro
       130                   135                   140

   Thr Val Gln Ala Thr Arg Ser Asn Tyr Thr Gln Ala His Arg Gly Ser
   145                   150                   155                   160

   Val Pro Pro Tyr Val Asp Tyr Phe Leu Gly Arg Gly Arg Gly Arg Val
                   165                   170                   175

   Leu Val Asp Val Leu Gln Ser Glu Gln Gly Ser Trp Phe Tyr Arg Lys
               180                   185                   190

   Arg Asn Arg Asn Met Val Val Glu Val Gln Glu Glu Val Pro Val Leu
               195                   200                   205

   Pro Asp Phe Cys Trp Leu Thr Leu Gly Gln Val Leu Ala Leu Leu Arg
       210                   215                   220

   Gln Asp Asn Ile Val Asn Met Asp Thr Arg Thr Val Leu Ser Cys Ile
   225                   230                   235                   240

   Pro Phe His Asp Ser Ala Thr Gly Pro Glu Leu Ala Ala Ser Glu Glu
                   245                   250                   255

   Pro Phe Arg Gln Ala Val Ala Arg Ser Leu Ser His Gly Ile Asp Ser
                   260                   265                   270

   Ser Ser Ile Ser Glu Ala Val Gly Trp Phe Glu Glu Ala Lys Ala Arg
           275                   280                   285

   Tyr Arg Leu Arg Ala Thr Arg Val Pro Leu Ser Arg Val Asp Lys Trp
       290                   295                   300

   Tyr Arg Thr Asp Thr Glu Ile Ala His Gln Asp Gly Lys Tyr Phe Ala
   305                   310                   315                   320

   Val Ile Ala Val Ser Val Ser Ala Thr Asn Arg Glu Val Ala Ser Trp
                   325                   330                   335

   Thr Gln Pro Met Ile Glu Pro Arg Glu Gln Gly Glu Ile Ala Leu Leu
```

```
        340                 345                 350

Val Lys Arg Ile Gly Gly Val Leu His Gly Leu Val His Ala Arg Val
        355                 360                 365

Glu Ala Gly Tyr Lys Trp Thr Ala Glu Ile Ala Pro Thr Val Gln Cys
    370                 375                 380

Ser Val Ala Asn Tyr Gln Ser Thr Pro Ser Asn Asp Trp Pro Pro Phe
385                 390                 395                 400

Leu Asp Asp Val Leu Thr Ala Asp Pro Glu Thr Val Arg Tyr Glu Ser
                405                 410                 415

Ile Leu Ser Glu Glu Gly Gly Arg Phe Tyr Gln Ala Gln Asn Arg Tyr
            420                 425                 430

Arg Ile Ile Glu Val His Glu Asp Phe Ala Ala Arg Pro Pro Ser Asp
        435                 440                 445

Phe Arg Trp Met Thr Leu Gly Gln Leu Gly Glu Leu Leu Arg Ser Thr
    450                 455                 460

His Phe Leu Asn Ile Gln Ala Arg Ser Leu Val Ala Ser Leu His Ser
465                 470                 475                 480

Leu Trp Ala Leu Gly Arg
                485
```

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<210> 27
<211> 524
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(438)
<223> ORF11; Thioesterase

<400> 27
gtg agc aac gtg tgg ccg gaa aca tgg acg ccg ggg ttt ggc agg tgt    48
Val Ser Asn Val Trp Pro Glu Thr Trp Thr Pro Gly Phe Gly Arg Cys
 1               5                   10                  15

tca tcg ctg ttg cgt cga ctc gga ttc cgc cgt gac cgg gac gat gcc    96
Ser Ser Leu Leu Arg Arg Leu Gly Phe Arg Arg Asp Arg Asp Asp Ala
```

```
                20                      25                      30

    agg cga gtc ccg aag tca gat tct tgt cca gaa tcg tcc aat ggg gtg    144
    Arg Arg Val Pro Lys Ser Asp Ser Cys Pro Glu Ser Ser Asn Gly Val
            35                      40                      45


    ttg atc tcc cca gag gtt tgc gct cca acc gat ttc cga cga gga tcg    192
    Leu Ile Ser Pro Glu Val Cys Ala Pro Thr Asp Phe Arg Arg Gly Ser
            50                      55                      60


    tgg cgc ccg ctg agc aac gac tac cgt gcg gtc gag aca tac cgc tgt    240
    Trp Arg Pro Leu Ser Asn Asp Tyr Arg Ala Val Glu Thr Tyr Arg Cys
    65                      70                      75                  80


    gcg cca gga gcg aag gtg ggt tgc ccg atc acc gtg ctg gtg gta gat    288
    Ala Pro Gly Ala Lys Val Gly Cys Pro Ile Thr Val Leu Val Val Asp
                        85                      90                      95


    gcc gag ccg aag gtc acc ttg gat gag gcg gaa gcc tgg cga gag cac    336
    Ala Glu Pro Lys Val Thr Leu Asp Glu Ala Glu Ala Trp Arg Glu His
                    100                     105                     110


    acc gag gcc gtg gcc gac gtc cgt gtc ttc tcc ggc ggg cat ttc ttc    384
    Thr Glu Ala Val Ala Asp Val Arg Val Phe Ser Gly Gly His Phe Phe
                115                     120                     125


    atg acc gaa cgc cag gac gag gtg ctc gcg gtc ctt acg ggc gga tcg    432
    Met Thr Glu Arg Gln Asp Glu Val Leu Ala Val Leu Thr Gly Gly Ser
        130                     135                     140


    ctt cga tgatcctcgc caggccgctg gaccagaccg cgacgcccct gggagccggc    488
    Leu Arg
    145


    gtgcacatcg tcacggcagt gagggattgg gcatga                            524



    <210> 28
    <211> 146
    <212> PRT
    <213> Saccharopolyspora spinosa


    <400> 28
    Val Ser Asn Val Trp Pro Glu Thr Trp Thr Pro Gly Phe Gly Arg Cys
    1               5                       10                      15


    Ser Ser Leu Leu Arg Arg Leu Gly Phe Arg Arg Asp Arg Asp Asp Ala
                20                      25                      30
```

```
Arg Arg Val Pro Lys Ser Asp Ser Cys Pro Glu Ser Ser Asn Gly Val
            35              40              45

Leu Ile Ser Pro Glu Val Cys Ala Pro Thr Asp Phe Arg Arg Gly Ser
        50              55              60

Trp Arg Pro Leu Ser Asn Asp Tyr Arg Ala Val Glu Thr Tyr Arg Cys
 65              70              75              80

Ala Pro Gly Ala Lys Val Gly Cys Pro Ile Thr Val Leu Val Val Asp
                85              90              95

Ala Glu Pro Lys Val Thr Leu Asp Glu Ala Glu Ala Trp Arg Glu His
            100             105             110

Thr Glu Ala Val Ala Asp Val Arg Val Phe Ser Gly Gly His Phe Phe
        115             120             125

Met Thr Glu Arg Gln Asp Glu Val Leu Ala Val Leu Thr Gly Gly Ser
    130             135             140

Leu Arg
145
```

```
<210> 29
<211> 1320
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(1317)
<223> ORF12; Glycosyltransferase

<400> 29
atg cgt gtc ctg ttc acc ccg ctg ccg gcg agt tcg cac ttc ttc aac    48
Met Arg Val Leu Phe Thr Pro Leu Pro Ala Ser Ser His Phe Phe Asn
 1               5                  10                  15

ctg gtg ccg ttg gcg tgg gcg ttg cgt gcc gcg ggg cac gag gtc cgt    96
Leu Val Pro Leu Ala Trp Ala Leu Arg Ala Ala Gly His Glu Val Arg
                20                  25                  30

gtc gcc atc tgc ccg aat atg gtg tcg atg gtc acc gga gca gga ctc   144
Val Ala Ile Cys Pro Asn Met Val Ser Met Val Thr Gly Ala Gly Leu
```

130

```
         35                    40                    45

acc gcg gtt ccc gtc ggc gac gag ctc gac ctc atc tcc ttg gcg gcc    192
Thr Ala Val Pro Val Gly Asp Glu Leu Asp Leu Ile Ser Leu Ala Ala
     50                     55                 60

aag aac gaa ctc gtt ctc ggc agc ggg gtc tcg ttc gac gag aag ggg    240
Lys Asn Glu Leu Val Leu Gly Ser Gly Val Ser Phe Asp Glu Lys Gly
 65                     70                 75                 80

cgg cat ccg gaa ctc ttc gac gag ctg ctg tca atc aac tcc ggc aga    288
Arg His Pro Glu Leu Phe Asp Glu Leu Leu Ser Ile Asn Ser Gly Arg
                 85                 90                 95

gac acg gac gcc gtg gag caa ctc cac ctt gtg gat gac cga tcg ctg    336
Asp Thr Asp Ala Val Glu Gln Leu His Leu Val Asp Asp Arg Ser Leu
             100                105                110

gac gat ctc atg ggg ttc gcc gag aaa tgg cag cct gat ctc gtt gtg    384
Asp Asp Leu Met Gly Phe Ala Glu Lys Trp Gln Pro Asp Leu Val Val
             115                120                125

tgg gac gct atg gtg tgt tcg ggg cca gtt gtg gcg cga gcg ctc ggc    432
Trp Asp Ala Met Val Cys Ser Gly Pro Val Val Ala Arg Ala Leu Gly
     130                135                140

gca cga cac gtg cgg atg ctc gtc gcc ctc gat gtg tcg ggg tgg ctg    480
Ala Arg His Val Arg Met Leu Val Ala Leu Asp Val Ser Gly Trp Leu
145                150                155                160

cgg tcc ggt ttc ctc gaa tac cag gaa tcg aag ccg cct gag cag cgc    528
Arg Ser Gly Phe Leu Glu Tyr Gln Glu Ser Lys Pro Pro Glu Gln Arg
                 165                170                175

gtc gac ccg ctc ggg acg tgg ctg gga gcg aag ctc gcc aag ttc gga    576
Val Asp Pro Leu Gly Thr Trp Leu Gly Ala Lys Leu Ala Lys Phe Gly
             180                185                190

gcc acg ttc gat gaa gag atc gtg acg ggc caa gcg acc ata gat ccg    624
Ala Thr Phe Asp Glu Glu Ile Val Thr Gly Gln Ala Thr Ile Asp Pro
             195                200                205

att cca tcc tgg atg cgc ctg cct gtg gac ttg gac tac atc tcg atg    672
Ile Pro Ser Trp Met Arg Leu Pro Val Asp Leu Asp Tyr Ile Ser Met
     210                215                220

cgt ttc gtg ccg tac aac ggt ccg gcg gtg ttg ccg gag tgg ttg cgc    720
Arg Phe Val Pro Tyr Asn Gly Pro Ala Val Leu Pro Glu Trp Leu Arg
```

```
        225                  230                  235                  240

        gaa cga ccg acg aag ccg cgc gtc tgc atc acg cgc ggg ctg acc aag    768
        Glu Arg Pro Thr Lys Pro Arg Val Cys Ile Thr Arg Gly Leu Thr Lys
                        245                  250                  255

        cgg cgg ctg agc agg gtg acc gaa cag tac ggg gag caa agt gac cag    816
        Arg Arg Leu Ser Arg Val Thr Glu Gln Tyr Gly Glu Gln Ser Asp Gln
                        260                  265                  270

        gaa caa gca atg gtg gaa agg ttg ttg cgc ggc gcg gcc agg ctc gac    864
        Glu Gln Ala Met Val Glu Arg Leu Leu Arg Gly Ala Ala Arg Leu Asp
                        275                  280                  285

        gtc gag gtg atc gcc acc ttg tct gac gac gaa gta cgg gag atg ggg    912
        Val Glu Val Ile Ala Thr Leu Ser Asp Asp Glu Val Arg Glu Met Gly
                290                  295                  300

        gag ttg ccc tcg aac gtc cgg gtc cac gaa tac gta ccg ctc aac gaa    960
        Glu Leu Pro Ser Asn Val Arg Val His Glu Tyr Val Pro Leu Asn Glu
        305                  310                  315                  320

        ctg ctg gag tcg tgt tca gtg atc atc cat cat ggc tcg acg acg acg   1008
        Leu Leu Glu Ser Cys Ser Val Ile Ile His His Gly Ser Thr Thr Thr
                        325                  330                  335

        cag gaa acc gcc acg gtc aac ggc gta ccg cag ttg att ctc cct ggg   1056
        Gln Glu Thr Ala Thr Val Asn Gly Val Pro Gln Leu Ile Leu Pro Gly
                        340                  345                  350

        acc ttc tgg gac gaa tct cgt agg gcg gag ctc cta gcc gat cgg gga   1104
        Thr Phe Trp Asp Glu Ser Arg Arg Ala Glu Leu Leu Ala Asp Arg Gly
                        355                  360                  365

        gcc ggt ctg gtc ctc gac ccc gcg acg ttt acc gaa gac gac gtg cga   1152
        Ala Gly Leu Val Leu Asp Pro Ala Thr Phe Thr Glu Asp Asp Val Arg
                370                  375                  380

        ggt cag ctg gcc cgc ctg ctc gac gag ccg tcg ttc gct gcc aac gcg   1200
        Gly Gln Leu Ala Arg Leu Leu Asp Glu Pro Ser Phe Ala Ala Asn Ala
        385                  390                  395                  400

        gcg ctg atc cgc cgt gaa atc gag gaa agt ccc agc ccg cac gac atc   1248
        Ala Leu Ile Arg Arg Glu Ile Glu Glu Ser Pro Ser Pro His Asp Ile
                        405                  410                  415

        gtt cca cgt ctg gaa aag cta gtt gcc gaa cgt gag aac cgc cgc act   1296
        Val Pro Arg Leu Glu Lys Leu Val Ala Glu Arg Glu Asn Arg Arg Thr
```

```
                420                  425                     430

ggg cag tct gat ggc cat ccg tga                              1320
Gly Gln Ser Asp Gly His Pro
        435
```

<210> 30
<211> 439
<212> PRT
<213> Saccharopolyspora spinosa

<400> 30

```
Met Arg Val Leu Phe Thr Pro Leu Pro Ala Ser Ser His Phe Phe Asn
 1               5                  10                  15

Leu Val Pro Leu Ala Trp Ala Leu Arg Ala Ala Gly His Glu Val Arg
            20                  25                  30

Val Ala Ile Cys Pro Asn Met Val Ser Met Val Thr Gly Ala Gly Leu
         35                  40                  45

Thr Ala Val Pro Val Gly Asp Glu Leu Asp Leu Ile Ser Leu Ala Ala
      50                  55                  60

Lys Asn Glu Leu Val Leu Gly Ser Gly Val Ser Phe Asp Glu Lys Gly
 65                  70                  75                  80

Arg His Pro Glu Leu Phe Asp Glu Leu Leu Ser Ile Asn Ser Gly Arg
               85                  90                  95

Asp Thr Asp Ala Val Glu Gln Leu His Leu Val Asp Asp Arg Ser Leu
            100                 105                 110

Asp Asp Leu Met Gly Phe Ala Glu Lys Trp Gln Pro Asp Leu Val Val
            115                 120                 125

Trp Asp Ala Met Val Cys Ser Gly Pro Val Val Ala Arg Ala Leu Gly
         130                 135                 140

Ala Arg His Val Arg Met Leu Val Ala Leu Asp Val Ser Gly Trp Leu
145                 150                 155                 160

Arg Ser Gly Phe Leu Glu Tyr Gln Glu Ser Lys Pro Pro Glu Gln Arg
               165                 170                 175

Val Asp Pro Leu Gly Thr Trp Leu Gly Ala Lys Leu Ala Lys Phe Gly
            180                 185                 190
```

```
Ala Thr Phe Asp Glu Glu Ile Val Thr Gly Gln Ala Thr Ile Asp Pro
        195             200             205

Ile Pro Ser Trp Met Arg Leu Pro Val Asp Leu Asp Tyr Ile Ser Met
    210             215             220

Arg Phe Val Pro Tyr Asn Gly Pro Ala Val Leu Pro Glu Trp Leu Arg
225             230             235             240

Glu Arg Pro Thr Lys Pro Arg Val Cys Ile Thr Arg Gly Leu Thr Lys
            245             250             255

Arg Arg Leu Ser Arg Val Thr Glu Gln Tyr Gly Glu Gln Ser Asp Gln
            260             265             270

Glu Gln Ala Met Val Glu Arg Leu Leu Arg Gly Ala Ala Arg Leu Asp
            275             280             285

Val Glu Val Ile Ala Thr Leu Ser Asp Asp Glu Val Arg Glu Met Gly
    290             295             300

Glu Leu Pro Ser Asn Val Arg Val His Glu Tyr Val Pro Leu Asn Glu
305             310             315             320

Leu Leu Glu Ser Cys Ser Val Ile Ile His His Gly Ser Thr Thr Thr
            325             330             335

Gln Glu Thr Ala Thr Val Asn Gly Val Pro Gln Leu Ile Leu Pro Gly
            340             345             350

Thr Phe Trp Asp Glu Ser Arg Arg Ala Glu Leu Leu Ala Asp Arg Gly
        355             360             365

Ala Gly Leu Val Leu Asp Pro Ala Thr Phe Thr Glu Asp Asp Val Arg
    370             375             380

Gly Gln Leu Ala Arg Leu Leu Asp Glu Pro Ser Phe Ala Ala Asn Ala
385             390             395             400

Ala Leu Ile Arg Arg Glu Ile Glu Glu Ser Pro Ser Pro His Asp Ile
            405             410             415

Val Pro Arg Leu Glu Lys Leu Val Ala Glu Arg Glu Asn Arg Arg Thr
        420             425             430

Gly Gln Ser Asp Gly His Pro
    435
```

<210> 31
<211> 1389
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(1386)
<223> ORF13; 3,4-Dehydratase

<400> 31

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atg cag agc cgg aaa acc aga gcg ctg ggg aaa ggg cgc gcc aga gtg    48
Met Gln Ser Arg Lys Thr Arg Ala Leu Gly Lys Gly Arg Ala Arg Val
 1               5                  10                  15


act tcg tgt gac gac act tgc gct acc gct act gag atg gtg ccg gat    96
Thr Ser Cys Asp Asp Thr Cys Ala Thr Ala Thr Glu Met Val Pro Asp
                20                  25                  30


gcc aag gac cgg ata ttg gca tcc gta cgc gat tac cac cgc gaa cag   144
Ala Lys Asp Arg Ile Leu Ala Ser Val Arg Asp Tyr His Arg Glu Gln
             35                  40                  45


gaa tcc ccg acc ttc gtg gct gga tcg acg ccg atc cgg cca tcg ggc   192
Glu Ser Pro Thr Phe Val Ala Gly Ser Thr Pro Ile Arg Pro Ser Gly
         50                  55                  60


gcc gtg ctc gac gag gac gac cgg gtg gca ctg gtg gaa gcc gcg ctg   240
Ala Val Leu Asp Glu Asp Asp Arg Val Ala Leu Val Glu Ala Ala Leu
 65                  70                  75                  80


gag ctc cgg atc gcc gcg ggc ggg aat gca cgg cga ttc gag agc gag   288
Glu Leu Arg Ile Ala Ala Gly Gly Asn Ala Arg Arg Phe Glu Ser Glu
                 85                  90                  95


ttc gcc cgc ttc ttc ggc ctc cgc aag gct cat ctc gtc aac tcc ggt   336
Phe Ala Arg Phe Phe Gly Leu Arg Lys Ala His Leu Val Asn Ser Gly
                100                 105                 110


tcg tcg gcc aat ctc ctg gca ctg agt tcg ctt acc tcc ccc aaa ctc   384
Ser Ser Ala Asn Leu Leu Ala Leu Ser Ser Leu Thr Ser Pro Lys Leu
            115                 120                 125


ggc gag gca cga ctg cgg ccc ggc gac gaa gtg atc act gcg gcg gtc   432
Gly Glu Ala Arg Leu Arg Pro Gly Asp Glu Val Ile Thr Ala Ala Val
```

```
          130                  135                  140

ggc ttc ccc acg acg atc aat ccg gcg gtc caa aac gga ctc gtc ccg      480
Gly Phe Pro Thr Thr Ile Asn Pro Ala Val Gln Asn Gly Leu Val Pro
145                 150                 155                 160

gta ttc gtc gac gtg gaa ctg ggc acc tac aac gca acg cca gac cgc      528
Val Phe Val Asp Val Glu Leu Gly Thr Tyr Asn Ala Thr Pro Asp Arg
                    165                 170                 175

atc aag gcc gcc gtc acg gaa cgg acg cga gcc atc atg ctg gcg cac      576
Ile Lys Ala Ala Val Thr Glu Arg Thr Arg Ala Ile Met Leu Ala His
                180                 185                 190

acc ctg ggc aac ccc ttc gcc gct gac gaa atc gcg gag atc gca aaa      624
Thr Leu Gly Asn Pro Phe Ala Ala Asp Glu Ile Ala Glu Ile Ala Lys
                195                 200                 205

gaa cac gag ctg ttc ctc gtc gaa gac aac tgt gat gcg gtg gga tcc      672
Glu His Glu Leu Phe Leu Val Glu Asp Asn Cys Asp Ala Val Gly Ser
            210                 215                 220

acc tac cgg gga cgg ctg acc gga acc ttc ggc gac ctg aca acg gtc      720
Thr Tyr Arg Gly Arg Leu Thr Gly Thr Phe Gly Asp Leu Thr Thr Val
225                 230                 235                 240

agc ttc tat cct gcc cat cac atc acc agc ggc gag ggt ggc tgc gtg      768
Ser Phe Tyr Pro Ala His His Ile Thr Ser Gly Glu Gly Gly Cys Val
                    245                 250                 255

ttg acc ggc agc ctg gaa ttg gct cgc atc atc gag tcg ctg cgt gac      816
Leu Thr Gly Ser Leu Glu Leu Ala Arg Ile Ile Glu Ser Leu Arg Asp
                260                 265                 270

tgg gga cgg gat tgc tgg tgc gag ccc ggc gtg gac aac acc tgc cgc      864
Trp Gly Arg Asp Cys Trp Cys Glu Pro Gly Val Asp Asn Thr Cys Arg
                275                 280                 285

aag agg ttc gac tac cac ctc ggt acc ctt cca ccg ggc tac gac cac      912
Lys Arg Phe Asp Tyr His Leu Gly Thr Leu Pro Pro Gly Tyr Asp His
                290                 295                 300

aag tac acg ttc tcc cac gtc ggt tac aac ctc aag acc acc gac ctg      960
Lys Tyr Thr Phe Ser His Val Gly Tyr Asn Leu Lys Thr Thr Asp Leu
305                 310                 315                 320

cag gcc gca ctt gcg ctg agc cag ttg agc aag att tcc gca ttc ggg     1008
Gln Ala Ala Leu Ala Leu Ser Gln Leu Ser Lys Ile Ser Ala Phe Gly
```

```
                    325                 330                 335

tcg gca cgc cgc cgt aac tgg cga cgg ttg cgc gaa ggg ctg tcc ggg    1056
Ser Ala Arg Arg Arg Asn Trp Arg Arg Leu Arg Glu Gly Leu Ser Gly
            340                 345                 350

ttg ccg ggc ctg ctg ctg ccg gta gcc aca ccg cac agc gac ccg agc    1104
Leu Pro Gly Leu Leu Leu Pro Val Ala Thr Pro His Ser Asp Pro Ser
            355                 360                 365

tgg ttc ggg ttt gcg atc acc atc agt gcg gac gcc ggg ttc acc cgt    1152
Trp Phe Gly Phe Ala Ile Thr Ile Ser Ala Asp Ala Gly Phe Thr Arg
            370                 375                 380

gcc gcc ctg gtg aac ttc ctg gaa tcc cgc aac atc ggc acc cga ctg    1200
Ala Ala Leu Val Asn Phe Leu Glu Ser Arg Asn Ile Gly Thr Arg Leu
385                 390                 395                 400

ctg ttc ggc ggt aac atc acc cgg cac ccg gcc ttc gag cag gtg cgg    1248
Leu Phe Gly Gly Asn Ile Thr Arg His Pro Ala Phe Glu Gln Val Arg
                405                 410                 415

tac cgg atc gcc gac gcg ctc acc aac agc gac atc gtc acc gac cga    1296
Tyr Arg Ile Ala Asp Ala Leu Thr Asn Ser Asp Ile Val Thr Asp Arg
            420                 425                 430

acc ttc tgg gtc ggc gtc tac cca ggc ata acg gac caa atg atc gac    1344
Thr Phe Trp Val Gly Val Tyr Pro Gly Ile Thr Asp Gln Met Ile Asp
            435                 440                 445

tac gtc gtc gaa tca atc gct gaa ttc gtg gcc aag agt tcc tag       1389
Tyr Val Val Glu Ser Ile Ala Glu Phe Val Ala Lys Ser Ser
    450                 455                 460
```

<210> 32
<211> 462
<212> PRT
<213> Saccharopolyspora spinosa

<400> 32

```
Met Gln Ser Arg Lys Thr Arg Ala Leu Gly Lys Gly Arg Ala Arg Val
 1               5                  10                  15

Thr Ser Cys Asp Asp Thr Cys Ala Thr Ala Thr Glu Met Val Pro Asp
            20                  25                  30

Ala Lys Asp Arg Ile Leu Ala Ser Val Arg Asp Tyr His Arg Glu Gln
```

```
              35                    40                    45

    Glu Ser Pro Thr Phe Val Ala Gly Ser Thr Pro Ile Arg Pro Ser Gly
          50                    55                    60

    Ala Val Leu Asp Glu Asp Asp Arg Val Ala Leu Val Glu Ala Ala Leu
    65                    70                    75                    80

    Glu Leu Arg Ile Ala Ala Gly Gly Asn Ala Arg Arg Phe Glu Ser Glu
                      85                    90                    95

    Phe Ala Arg Phe Phe Gly Leu Arg Lys Ala His Leu Val Asn Ser Gly
                  100                   105                   110

    Ser Ser Ala Asn Leu Leu Ala Leu Ser Ser Leu Thr Ser Pro Lys Leu
              115                   120                   125

    Gly Glu Ala Arg Leu Arg Pro Gly Asp Glu Val Ile Thr Ala Ala Val
          130                   135                   140

    Gly Phe Pro Thr Thr Ile Asn Pro Ala Val Gln Asn Gly Leu Val Pro
    145                   150                   155                   160

    Val Phe Val Asp Val Glu Leu Gly Thr Tyr Asn Ala Thr Pro Asp Arg
                  165                   170                   175

    Ile Lys Ala Ala Val Thr Glu Arg Thr Arg Ala Ile Met Leu Ala His
              180                   185                   190

    Thr Leu Gly Asn Pro Phe Ala Ala Asp Glu Ile Ala Glu Ile Ala Lys
              195                   200                   205

    Glu His Glu Leu Phe Leu Val Glu Asp Asn Cys Asp Ala Val Gly Ser
          210                   215                   220

    Thr Tyr Arg Gly Arg Leu Thr Gly Thr Phe Gly Asp Leu Thr Thr Val
    225                   230                   235                   240

    Ser Phe Tyr Pro Ala His His Ile Thr Ser Gly Glu Gly Gly Cys Val
                  245                   250                   255

    Leu Thr Gly Ser Leu Glu Leu Ala Arg Ile Ile Glu Ser Leu Arg Asp
              260                   265                   270

    Trp Gly Arg Asp Cys Trp Cys Glu Pro Gly Val Asp Asn Thr Cys Arg
              275                   280                   285

    Lys Arg Phe Asp Tyr His Leu Gly Thr Leu Pro Pro Gly Tyr Asp His
```

138

```
        290                    295                    300
Lys Tyr Thr Phe Ser His Val Gly Tyr Asn Leu Lys Thr Thr Asp Leu
305                    310                    315                    320

Gln Ala Ala Leu Ala Leu Ser Gln Leu Ser Lys Ile Ser Ala Phe Gly
                325                    330                    335

Ser Ala Arg Arg Arg Asn Trp Arg Arg Leu Arg Glu Gly Leu Ser Gly
                340                    345                    350

Leu Pro Gly Leu Leu Leu Pro Val Ala Thr Pro His Ser Asp Pro Ser
                355                    360                    365

Trp Phe Gly Phe Ala Ile Thr Ile Ser Ala Asp Ala Gly Phe Thr Arg
        370                    375                    380

Ala Ala Leu Val Asn Phe Leu Glu Ser Arg Asn Ile Gly Thr Arg Leu
385                    390                    395                    400

Leu Phe Gly Gly Asn Ile Thr Arg His Pro Ala Phe Glu Gln Val Arg
                405                    410                    415

Tyr Arg Ile Ala Asp Ala Leu Thr Asn Ser Asp Ile Val Thr Asp Arg
                420                    425                    430

Thr Phe Trp Val Gly Val Tyr Pro Gly Ile Thr Asp Gln Met Ile Asp
                435                    440                    445

Tyr Val Val Glu Ser Ile Ala Glu Phe Val Ala Lys Ser Ser
        450                    455                    460
```

```
<210> 33
<211> 1158
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(1155)
<223> ORF14; 4-Aminotransferase

<400> 33
gtg atc aac ctg cac cag ccg atc ctc ggc acc gaa gaa ctc gac gcg     48
Val Ile Asn Leu His Gln Pro Ile Leu Gly Thr Glu Glu Leu Asp Ala
 1               5                    10                   15
```

```
atc gcg gag gtg ttc gcc tcc aac tgg atc ggg ctc ggg ccg cgc acc   96
Ile Ala Glu Val Phe Ala Ser Asn Trp Ile Gly Leu Gly Pro Arg Thr
            20                  25                  30

cgg acg ttc gag gcc gaa ttc gcc cac cac ctg gga gtg gat ccc gaa  144
Arg Thr Phe Glu Ala Glu Phe Ala His His Leu Gly Val Asp Pro Glu
            35                  40                  45

cag gtc gtg ttc ctc aac tcg ggg act gcc gcg ctg ttc ctt acc gtg  192
Gln Val Val Phe Leu Asn Ser Gly Thr Ala Ala Leu Phe Leu Thr Val
        50                  55                  60

cag gtg ctc gac ctc ggc cca ggc gac gac gtg gta ctt cct tcg ata  240
Gln Val Leu Asp Leu Gly Pro Gly Asp Asp Val Val Leu Pro Ser Ile
65                  70                  75                  80

agc ttc gtg gcg gcg gcc aac gcc atc gca tcc tcc ggt gcc cgc ccg  288
Ser Phe Val Ala Ala Ala Asn Ala Ile Ala Ser Ser Gly Ala Arg Pro
                85                  90                  95

gtg ttc tgc gac gtc gac ccc cgg acg ttg aac ccc acg ctg gat gat  336
Val Phe Cys Asp Val Asp Pro Arg Thr Leu Asn Pro Thr Leu Asp Asp
            100                 105                 110

gtg gcg agg gcc atc acg ccg gcg acc aag gcc gta ttg ctg ctc cac  384
Val Ala Arg Ala Ile Thr Pro Ala Thr Lys Ala Val Leu Leu Leu His
            115                 120                 125

tat gga gga tcg ccg gga gaa gtc acc gcg atc gcc gat ttc tgc cgt  432
Tyr Gly Gly Ser Pro Gly Glu Val Thr Ala Ile Ala Asp Phe Cys Arg
        130                 135                 140

gaa aag ggc ctc atg ctc atc gag gac tcc gcc tgc gcg gtg gca tcg  480
Glu Lys Gly Leu Met Leu Ile Glu Asp Ser Ala Cys Ala Val Ala Ser
145                 150                 155                 160

tcc gtg cac ggc acc gct tgc gga acc ttt ggt gac ctg gcc acg tgg  528
Ser Val His Gly Thr Ala Cys Gly Thr Phe Gly Asp Leu Ala Thr Trp
                165                 170                 175

agt ttc gat gcg atg aag atc ctg gtc acc ggg gat ggg ggc atg ttc  576
Ser Phe Asp Ala Met Lys Ile Leu Val Thr Gly Asp Gly Gly Met Phe
            180                 185                 190

tac gcg gcg gat ccg gag ctg gcg cac cgc gca aga cga ctc gcc tac  624
Tyr Ala Ala Asp Pro Glu Leu Ala His Arg Ala Arg Arg Leu Ala Tyr
            195                 200                 205
```

```
cac ggt ctt gag cag atg agc gga ttc gat tcg gcc aag tct tcc aac    672
His Gly Leu Glu Gln Met Ser Gly Phe Asp Ser Ala Lys Ser Ser Asn
    210                 215                 220

cgc tgg tgg gat att cgc gtc gaa gac atc ggc cag cgg ctg atc ggg    720
Arg Trp Trp Asp Ile Arg Val Glu Asp Ile Gly Gln Arg Leu Ile Gly
225                 230                 235                 240

aac gac atg acg gca gcg ctt ggc agc gtg cag ctg cgc aaa ctg cca    768
Asn Asp Met Thr Ala Ala Leu Gly Ser Val Gln Leu Arg Lys Leu Pro
                245                 250                 255

gaa ttc atc aac agg cgt aga gaa atc gct acg cag tac gac cgg ttg    816
Glu Phe Ile Asn Arg Arg Arg Glu Ile Ala Thr Gln Tyr Asp Arg Leu
                260                 265                 270

ctt tcc gat gtg ccg ggt gtc ctc cta ccg ccg acg cta ccg gat ggg    864
Leu Ser Asp Val Pro Gly Val Leu Leu Pro Pro Thr Leu Pro Asp Gly
                275                 280                 285

cac gtc tcg tca cac tac ttc tac tgg gtc cag ctg gct ccg gag atc    912
His Val Ser Ser His Tyr Phe Tyr Trp Val Gln Leu Ala Pro Glu Ile
    290                 295                 300

cgc gac cag gtg gcg cag caa atg ctg gaa cgc ggc atc tac acg agc    960
Arg Asp Gln Val Ala Gln Gln Met Leu Glu Arg Gly Ile Tyr Thr Ser
305                 310                 315                 320

tac cgc tac ccg ccc ctg cac aag gtc ccc atc tac cgc gcg gac tgc   1008
Tyr Arg Tyr Pro Pro Leu His Lys Val Pro Ile Tyr Arg Ala Asp Cys
                325                 330                 335

aag ctg cct tct gcg gag cac gcc tgc cgc aga aca ctc ctg cta cca   1056
Lys Leu Pro Ser Ala Glu His Ala Cys Arg Arg Thr Leu Leu Leu Pro
                340                 345                 350

ctg cac cca agc ctt gac gac gcc gag gtg cgc acg gtg gct gac gag   1104
Leu His Pro Ser Leu Asp Asp Ala Glu Val Arg Thr Val Ala Asp Glu
                355                 360                 365

ttc cag aag gcc gtc gaa cac cac atc agc caa aga tca cca ctc cga   1152
Phe Gln Lys Ala Val Glu His His Ile Ser Gln Arg Ser Pro Leu Arg
    370                 375                 380

aag tga                                                            1158
Lys
385
```

<210> 34
<211> 385
<212> PRT
<213> Saccharopolyspora spinosa

<400> 34
Val Ile Asn Leu His Gln Pro Ile Leu Gly Thr Glu Glu Leu Asp Ala
 1   5   10   15

Ile Ala Glu Val Phe Ala Ser Asn Trp Ile Gly Leu Gly Pro Arg Thr
                20   25   30

Arg Thr Phe Glu Ala Glu Phe Ala His His Leu Gly Val Asp Pro Glu
            35   40   45

Gln Val Val Phe Leu Asn Ser Gly Thr Ala Ala Leu Phe Leu Thr Val
        50   55   60

Gln Val Leu Asp Leu Gly Pro Gly Asp Asp Val Val Leu Pro Ser Ile
65   70   75   80

Ser Phe Val Ala Ala Ala Asn Ala Ile Ala Ser Ser Gly Ala Arg Pro
                85   90   95

Val Phe Cys Asp Val Asp Pro Arg Thr Leu Asn Pro Thr Leu Asp Asp
            100   105   110

Val Ala Arg Ala Ile Thr Pro Ala Thr Lys Ala Val Leu Leu Leu His
        115   120   125

Tyr Gly Gly Ser Pro Gly Glu Val Thr Ala Ile Ala Asp Phe Cys Arg
    130   135   140

Glu Lys Gly Leu Met Leu Ile Glu Asp Ser Ala Cys Ala Val Ala Ser
145   150   155   160

Ser Val His Gly Thr Ala Cys Gly Thr Phe Gly Asp Leu Ala Thr Trp
                165   170   175

Ser Phe Asp Ala Met Lys Ile Leu Val Thr Gly Asp Gly Gly Met Phe
                180   185   190

Tyr Ala Ala Asp Pro Glu Leu Ala His Arg Ala Arg Arg Leu Ala Tyr
    195   200   205

His Gly Leu Glu Gln Met Ser Gly Phe Asp Ser Ala Lys Ser Ser Asn

142

```
            210                     215                     220

    Arg Trp Trp Asp Ile Arg Val Glu Asp Ile Gly Gln Arg Leu Ile Gly
    225                 230                 235                 240

    Asn Asp Met Thr Ala Ala Leu Gly Ser Val Gln Leu Arg Lys Leu Pro
                    245                 250                 255

    Glu Phe Ile Asn Arg Arg Arg Glu Ile Ala Thr Gln Tyr Asp Arg Leu
                    260                 265                 270

    Leu Ser Asp Val Pro Gly Val Leu Leu Pro Pro Thr Leu Pro Asp Gly
                275                 280                 285

    His Val Ser Ser His Tyr Phe Tyr Trp Val Gln Leu Ala Pro Glu Ile
                290                 295                 300

    Arg Asp Gln Val Ala Gln Gln Met Leu Glu Arg Gly Ile Tyr Thr Ser
    305                 310                 315                 320

    Tyr Arg Tyr Pro Pro Leu His Lys Val Pro Ile Tyr Arg Ala Asp Cys
                    325                 330                 335

    Lys Leu Pro Ser Ala Glu His Ala Cys Arg Arg Thr Leu Leu Leu Pro
                    340                 345                 350

    Leu His Pro Ser Leu Asp Asp Ala Glu Val Arg Thr Val Ala Asp Glu
                    355                 360                 365

    Phe Gln Lys Ala Val Glu His His Ile Ser Gln Arg Ser Pro Leu Arg
                370                 375                 380

    Lys
    385
```

<210> 35
<211> 750
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(747)
<223> ORF15; N-Dimethyltransferase

<400> 35

```
atg tcg cgc gtg agc gac aca ttc gca gaa acc tcc tcg gta tac agc    48
Met Ser Arg Val Ser Asp Thr Phe Ala Glu Thr Ser Ser Val Tyr Ser
 1               5                   10                  15


cca gat cat gcc gac atc tac gac gcg atc cac tcc gcg cgt ggc cgg    96
Pro Asp His Ala Asp Ile Tyr Asp Ala Ile His Ser Ala Arg Gly Arg
            20                  25                  30


gac tgg gca gcc gag gcc ggg gaa gta gtc cag ctc gta cgc acc agg   144
Asp Trp Ala Ala Glu Ala Gly Glu Val Val Gln Leu Val Arg Thr Arg
            35                  40                  45


ctg ccc gaa gca cag tcc cta ctc gac gtc gcc tgt ggg acc ggg gcg   192
Leu Pro Glu Ala Gln Ser Leu Leu Asp Val Ala Cys Gly Thr Gly Ala
        50                  55                  60


cac cta gag cga ttc cgt gcc gaa tac gcg aag gtc gcg ggg ctt gaa   240
His Leu Glu Arg Phe Arg Ala Glu Tyr Ala Lys Val Ala Gly Leu Glu
65                  70                  75                  80


ctg tcc gat gcg atg cgg gag atc gcg atc aga cga gtc cct gag gta   288
Leu Ser Asp Ala Met Arg Glu Ile Ala Ile Arg Arg Val Pro Glu Val
                85                  90                  95


ccg att cac atc ggt gac atc cgc gat ttc gac ctc ggc gag cca ttc   336
Pro Ile His Ile Gly Asp Ile Arg Asp Phe Asp Leu Gly Glu Pro Phe
            100                 105                 110


gac gtc atc acc tgc ctg tgc ttt acc gcg gct tac atg cgg acc gtt   384
Asp Val Ile Thr Cys Leu Cys Phe Thr Ala Ala Tyr Met Arg Thr Val
            115                 120                 125


gac gac ctg cga cgc gtg acg cgg aac atg gcc cgg cac ctg gcc cct   432
Asp Asp Leu Arg Arg Val Thr Arg Asn Met Ala Arg His Leu Ala Pro
        130                 135                 140


ggt gga gtc gcg gtc atc gaa ccc tgg tgg ttt ccc gac aag ttc atc   480
Gly Gly Val Ala Val Ile Glu Pro Trp Trp Phe Pro Asp Lys Phe Ile
145                 150                 155                 160


gac ggg ttc gtc acc gga gcc gtc gcg cac cac ggc gag cgg gtg atc   528
Asp Gly Phe Val Thr Gly Ala Val Ala His His Gly Glu Arg Val Ile
                165                 170                 175


agc cgg cta tcg cac tcg gtc ctg gag ggc cgt acg agc cgg atg acc   576
Ser Arg Leu Ser His Ser Val Leu Glu Gly Arg Thr Ser Arg Met Thr
            180                 185                 190
```

```
gtc cgc tac aca gtc gcc gaa ccc acc ggg atc cgg gac ttc aca gag   624
Val Arg Tyr Thr Val Ala Glu Pro Thr Gly Ile Arg Asp Phe Thr Glu
        195                 200                 205

ttc gaa atc ctc tcg ctg ttc act gag gac gag tac acc gcc gcg ctc   672
Phe Glu Ile Leu Ser Leu Phe Thr Glu Asp Glu Tyr Thr Ala Ala Leu
        210                 215                 220

gaa gac gca ggg atc cgc gcg gaa tac ctt cct gga gca ccg aac ggc   720
Glu Asp Ala Gly Ile Arg Ala Glu Tyr Leu Pro Gly Ala Pro Asn Gly
225                 230                 235                 240

cga ggc ctg ttc gtc gga atc cgc aac tga                           750
Arg Gly Leu Phe Val Gly Ile Arg Asn
                245


<210> 36
<211> 249
<212> PRT
<213> Saccharopolyspora spinosa

<400> 36
Met Ser Arg Val Ser Asp Thr Phe Ala Glu Thr Ser Ser Val Tyr Ser
 1               5                  10                  15

Pro Asp His Ala Asp Ile Tyr Asp Ala Ile His Ser Ala Arg Gly Arg
            20                  25                  30

Asp Trp Ala Ala Glu Ala Gly Glu Val Val Gln Leu Val Arg Thr Arg
        35                  40                  45

Leu Pro Glu Ala Gln Ser Leu Leu Asp Val Ala Cys Gly Thr Gly Ala
    50                  55                  60

His Leu Glu Arg Phe Arg Ala Glu Tyr Ala Lys Val Ala Gly Leu Glu
65                  70                  75                  80

Leu Ser Asp Ala Met Arg Glu Ile Ala Ile Arg Arg Val Pro Glu Val
                85                  90                  95

Pro Ile His Ile Gly Asp Ile Arg Asp Phe Asp Leu Gly Glu Pro Phe
            100                 105                 110

Asp Val Ile Thr Cys Leu Cys Phe Thr Ala Ala Tyr Met Arg Thr Val
            115                 120                 125

Asp Asp Leu Arg Arg Val Thr Arg Asn Met Ala Arg His Leu Ala Pro
```

```
           130                  135                  140

Gly Gly Val Ala Val Ile Glu Pro Trp Trp Phe Pro Asp Lys Phe Ile
145                  150                  155                  160

Asp Gly Phe Val Thr Gly Ala Val Ala His His Gly Glu Arg Val Ile
                165                  170                  175

Ser Arg Leu Ser His Ser Val Leu Glu Gly Arg Thr Ser Arg Met Thr
                180                  185                  190

Val Arg Tyr Thr Val Ala Glu Pro Thr Gly Ile Arg Asp Phe Thr Glu
            195                  200                  205

Phe Glu Ile Leu Ser Leu Phe Thr Glu Asp Glu Tyr Thr Ala Ala Leu
        210                  215                  220

Glu Asp Ala Gly Ile Arg Ala Glu Tyr Leu Pro Gly Ala Pro Asn Gly
225                  230                  235                  240

Arg Gly Leu Phe Val Gly Ile Arg Asn
                245
```


```
<210> 37
<211> 726
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(723)
<223> ORF16; 3,4-Reduktase

<400> 37
atg agc gaa cag acg att gca ctg gtc acc ggc gca aac aag gga atc    48
Met Ser Glu Gln Thr Ile Ala Leu Val Thr Gly Ala Asn Lys Gly Ile
 1               5                  10                  15

gga tac gag atc gcg gcc ggg ctc ggc gcg ctg ggg tgg agc gtc gga    96
Gly Tyr Glu Ile Ala Ala Gly Leu Gly Ala Leu Gly Trp Ser Val Gly
            20                  25                  30

atc ggg gca cgg gac cac cag cgc ggg gag gat gcc gtg gcg aaa ttg   144
Ile Gly Ala Arg Asp His Gln Arg Gly Glu Asp Ala Val Ala Lys Leu
        35                  40                  45
```

cgt gcg gac ggc gtc gat gcg ttc gcg gta tcc ctg gac gtg aca gac   192
Arg Ala Asp Gly Val Asp Ala Phe Ala Val Ser Leu Asp Val Thr Asp
        50   55   60

gac gcg agc gtc gcg gct gct gcg gct ctg ctc gag gag cgc gcc ggc   240
Asp Ala Ser Val Ala Ala Ala Ala Ala Leu Leu Glu Glu Arg Ala Gly
    65   70   75   80

cgg ctc gat gtg ctg gtt aat aac gcc ggc atc gcc ggg gca tgg ccg   288
Arg Leu Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gly Ala Trp Pro
                85   90   95

gag gag ccc tcg acc gtc aca ccg gcg agc ctc cgg gcg gtg gtg gag   336
Glu Glu Pro Ser Thr Val Thr Pro Ala Ser Leu Arg Ala Val Val Glu
            100   105   110

acc aac gtg atc ggc gtc gtt cgg gtt acc aac gct atg ctg ccg ttg   384
Thr Asn Val Ile Gly Val Val Arg Val Thr Asn Ala Met Leu Pro Leu
            115   120   125

cta cgc cgc tcc gag cgc ccg cgg atc gtc aac cag tcc agc cac gtc   432
Leu Arg Arg Ser Glu Arg Pro Arg Ile Val Asn Gln Ser Ser His Val
        130   135   140

gct tcc ctg acc ttg caa acc acg ccg ggc gtc gac ctc ggc ggg atc   480
Ala Ser Leu Thr Leu Gln Thr Thr Pro Gly Val Asp Leu Gly Gly Ile
145   150   155   160

agc gga gcc tac tca ccg tcg aag acg ttc ctc aac gcg atc acc atc   528
Ser Gly Ala Tyr Ser Pro Ser Lys Thr Phe Leu Asn Ala Ile Thr Ile
                165   170   175

cag tac gcc aag gaa ctc agc gat acc aac atc aaa atc aac aac gcc   576
Gln Tyr Ala Lys Glu Leu Ser Asp Thr Asn Ile Lys Ile Asn Asn Ala
                180   185   190

tgc ccc ggc tac gtc gcg acc gac ctt aac ggc ttc cac gga acc agc   624
Cys Pro Gly Tyr Val Ala Thr Asp Leu Asn Gly Phe His Gly Thr Ser
            195   200   205

acg ccg gca gac ggt gcc agg atc gcc att cgg ctc gcc acg ctg cca   672
Thr Pro Ala Asp Gly Ala Arg Ile Ala Ile Arg Leu Ala Thr Leu Pro
        210   215   220

gac gac ggc ccg acc gga ggc atg ttc gac gac gcc ggg aat gtg ccc   720
Asp Asp Gly Pro Thr Gly Gly Met Phe Asp Asp Ala Gly Asn Val Pro
225   230   235   240

147

```
tgg tga                                                        726
Trp
```

<210> 38
<211> 241
<212> PRT
<213> Saccharopolyspora spinosa

<400> 38

```
Met Ser Glu Gln Thr Ile Ala Leu Val Thr Gly Ala Asn Lys Gly Ile
 1·              5                  10                  ·15

Gly Tyr Glu Ile Ala Ala Gly Leu Gly Ala Leu Gly Trp Ser Val Gly
            20                  25                  30

Ile Gly Ala Arg Asp His Gln Arg Gly Glu Asp Ala Val Ala Lys Leu
         35                  40                  45

Arg Ala Asp Gly Val Asp Ala Phe Ala Val Ser Leu Asp Val Thr Asp
     50                  55                  60

Asp Ala Ser Val Ala Ala Ala Ala Ala Leu Leu Glu Glu Arg Ala Gly
 65.                  70                  75                  80

Arg Leu Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gly Ala Trp Pro
                 85                  90                  95

Glu Glu Pro Ser Thr Val Thr Pro Ala Ser Leu Arg Ala Val Val Glu
                100                 105                 110

Thr Asn Val Ile Gly Val Val Arg Val Thr Asn Ala Met Leu Pro Leu
            115                 120                 125

Leu Arg Arg Ser Glu Arg Pro Arg Ile Val Asn Gln Ser Ser His Val
     130                 135                 140

Ala Ser Leu Thr Leu Gln Thr Thr Pro Gly Val Asp Leu Gly Gly Ile
145                 150                 155                 160

Ser Gly Ala Tyr Ser Pro Ser Lys Thr Phe Leu Asn Ala Ile Thr Ile
                165                 170                 175

Gln Tyr Ala Lys Glu Leu Ser Asp Thr Asn Ile Lys Ile Asn Asn Ala
                180                 185                 190

Cys Pro Gly Tyr Val Ala Thr Asp Leu Asn Gly Phe His Gly Thr Ser
            195                 200                 205
```

```
Thr Pro Ala Asp Gly Ala Arg Ile Ala Ile Arg Leu Ala Thr Leu Pro
    210                 215                 220

Asp Asp Gly Pro Thr Gly Gly Met Phe Asp Asp Ala Gly Asn Val Pro
225                 230                 235                 240

Trp
```

```
<210> 39
<211> 837
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(834)
<223> ORF17; Transkriptions-Regulator

<400> 39
atg gag acg cgg gag ttg cgg tac ttc gtt gca gtc gcc gag gag ttg    48
Met Glu Thr Arg Glu Leu Arg Tyr Phe Val Ala Val Ala Glu Glu Leu
  1               5                  10                  15

cac ttc ggc cgg gcc gcc cag cgc ctg ggc atc gcc cag ccg ccg ctg    96
His Phe Gly Arg Ala Ala Gln Arg Leu Gly Ile Ala Gln Pro Pro Leu
             20                  25                  30

tcg cgg acg atc gcc cag ctc gag caa cga ctc gga gtc gtg ttg ctg   144
Ser Arg Thr Ile Ala Gln Leu Glu Gln Arg Leu Gly Val Val Leu Leu
         35                  40                  45

caa cgc acc agc cgc aaa gtc tcg ctc acc gaa gcc ggg gca atg ctg   192
Gln Arg Thr Ser Arg Lys Val Ser Leu Thr Glu Ala Gly Ala Met Leu
     50                  55                  60

ctg acc gaa ggc cgg gcg atc ctc ggc gcg ctg gca gca gcc gag cga   240
Leu Thr Glu Gly Arg Ala Ile Leu Gly Ala Leu Ala Ala Ala Glu Arg
 65                  70                  75                  80

cgc acc cag cgt gcc gcg acg agc cag ccc tcg cta gtc ctg gct gcc   288
Arg Thr Gln Arg Ala Ala Thr Ser Gln Pro Ser Leu Val Leu Ala Ala
                 85                  90                  95

aag gcc ggc gcc tcc ggt gag ctg ctg gcg aag ttg ctc gac gcg tac   336
```

```
        Lys Ala Gly Ala Ser Gly Glu Leu Leu Ala Lys Leu Leu Asp Ala Tyr
                     100                 105                 110

gcc gcc gag ccg gga gcc gtg gcc gtc gac ctg ctg ctc tgc gaa tcc    384
Ala Ala Glu Pro Gly Ala Val Ala Val Asp Leu Leu Leu Cys Glu Ser
            115                 120                 125

cag ccc cag aaa acg ctg cat gac ggc cgg gcc gac gtg gcg ctg ttg    432
Gln Pro Gln Lys Thr Leu His Asp Gly Arg Ala Asp Val Ala Leu Leu
        130                 135                 140

cat caa ccc ttc gac ccg acg gcc gaa ctc gac atc gaa att ctg aac    480
His Gln Pro Phe Asp Pro Thr Ala Glu Leu Asp Ile Glu Ile Leu Asn
145                 150                 155                 160

acc gag caa caa gtc gcc att ctt ccg acc tcg cat ccg ctt gcc agc    528
Thr Glu Gln Gln Val Ala Ile Leu Pro Thr Ser His Pro Leu Ala Ser
                     165                 170                 175

gag ccc cat gta cgg atg gcg gat gtc agc tca ctg ccg gat ctc ccg    576
Glu Pro His Val Arg Met Ala Asp Val Ser Ser Leu Pro Asp Leu Pro
                180                 185                 190

ctt gcg cgc tgg ccc ggc ccc gac ggc gtc tat cca gat ggc ccc ggc    624
Leu Ala Arg Trp Pro Gly Pro Asp Gly Val Tyr Pro Asp Gly Pro Gly
            195                 200                 205

gtg gaa gta cgc aac cag acg caa ctg ttc caa atg atc gca ctc ggc    672
Val Glu Val Arg Asn Gln Thr Gln Leu Phe Gln Met Ile Ala Leu Gly
        210                 215                 220

cgc act acc gtg gtc atg ccc gaa tcc agt cgc gtc aac ctg ctc gaa    720
Arg Thr Thr Val Val Met Pro Glu Ser Ser Arg Val Asn Leu Leu Glu
225                 230                 235                 240

ggc ctc gcc gcc gta ccg gtt cta gac gcg ccg gac gtg acg aca gtc    768
Gly Leu Ala Ala Val Pro Val Leu Asp Ala Pro Asp Val Thr Thr Val
                     245                 250                 255

atc gcc tgg ccg ccc cac agc cgc tcc cga gca ctc gcc ggc ttg gtc    816
Ile Ala Trp Pro Pro His Ser Arg Ser Arg Ala Leu Ala Gly Leu Val
                260                 265                 270

cgc gtg gcc aca ctc ctc taa                                        837
Arg Val Ala Thr Leu Leu
            275
```

<210> 40
<211> 278
<212> PRT
<213> Saccharopolyspora spinosa

<400> 40
Met Glu Thr Arg Glu Leu Arg Tyr Phe Val Ala Val Ala Glu Glu Leu
 1   5   10   15

His Phe Gly Arg Ala Ala Gln Arg Leu Gly Ile Ala Gln Pro Pro Leu
            20   25   30

Ser Arg Thr Ile Ala Gln Leu Glu Gln Arg Leu Gly Val Val Leu Leu
        35   40   45

Gln Arg Thr Ser Arg Lys Val Ser Leu Thr Glu Ala Gly Ala Met Leu
     50   55   60

Leu Thr Glu Gly Arg Ala Ile Leu Gly Ala Leu Ala Ala Ala Glu Arg
65   70   75   80

Arg Thr Gln Arg Ala Ala Thr Ser Gln Pro Ser Leu Val Leu Ala Ala
                85   90   95

Lys Ala Gly Ala Ser Gly Glu Leu Leu Ala Lys Leu Leu Asp Ala Tyr
            100   105   110

Ala Ala Glu Pro Gly Ala Val Ala Val Asp Leu Leu Leu Cys Glu Ser
            115   120   125

Gln Pro Gln Lys Thr Leu His Asp Gly Arg Ala Asp Val Ala Leu Leu
     130   135   140

His Gln Pro Phe Asp Pro Thr Ala Glu Leu Asp Ile Glu Ile Leu Asn
145   150   155   160

Thr Glu Gln Gln Val Ala Ile Leu Pro Thr Ser His Pro Leu Ala Ser
                165   170   175

Glu Pro His Val Arg Met Ala Asp Val Ser Ser Leu Pro Asp Leu Pro
            180   185   190

Leu Ala Arg Trp Pro Gly Pro Asp Gly Val Tyr Pro Asp Gly Pro Gly
            195   200   205

Val Glu Val Arg Asn Gln Thr Gln Leu Phe Gln Met Ile Ala Leu Gly
     210   215   220

```
Arg Thr Thr Val Val Met Pro Glu Ser Ser Arg Val Asn Leu Leu Glu
225             230             235             240

Gly Leu Ala Ala Val Pro Val Leu Asp Ala Pro Asp Val Thr Thr Val
            245             250             255

Ile Ala Trp Pro Pro His Ser Arg Ser Arg Ala Leu Ala Gly Leu Val
            260             265             270

Arg Val Ala Thr Leu Leu
        275
```

```
<210> 41
<211> 7788
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(7785)
<223> ORF18; Polyketidsynthase

<400> 41
atg agc gaa gcc ggg aac ctg ata gcc gtc atc gga ctg tcc tgc cgc    48
Met Ser Glu Ala Gly Asn Leu Ile Ala Val Ile Gly Leu Ser Cys Arg
 1               5                  10                  15

cta ccc cag gcg cct gac ccg gct tcc ttc tgg cgg ttg ctg cgc acc    96
Leu Pro Gln Ala Pro Asp Pro Ala Ser Phe Trp Arg Leu Leu Arg Thr
                20                  25                  30

gga acg gac gcc atc acc acg gtc ccg gaa ggg cgg tgg ggc gac ccg   144
Gly Thr Asp Ala Ile Thr Thr Val Pro Glu Gly Arg Trp Gly Asp Pro
            35                  40                  45

ttg cct ggt cgg gat gcg ccc aag ggc ccg gaa tgg ggt ggt ttc ctg   192
Leu Pro Gly Arg Asp Ala Pro Lys Gly Pro Glu Trp Gly Gly Phe Leu
    50                  55                  60

gct gat gtc gac tgc ttc gat ccc gag ttc ttc ggg atc tcg ccg cga   240
Ala Asp Val Asp Cys Phe Asp Pro Glu Phe Phe Gly Ile Ser Pro Arg
65                  70                  75                  80

gaa gcg gca gcc gtg gat ccc cag cag agg ctg gct ctg gag ctc gcc   288
Glu Ala Ala Ala Val Asp Pro Gln Gln Arg Leu Ala Leu Glu Leu Ala
                85                  90                  95
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tgg gag gca ctc gaa gac gcc ggt atc ccc gcc ggc gag ctg cgc ggt      336
Trp Glu Ala Leu Glu Asp Ala Gly Ile Pro Ala Gly Glu Leu Arg Gly
            100             105             110

act gcc gcc ggt gtg ttc atg ggg gcg atc tct gac gac tac gcc gcc      384
Thr Ala Ala Gly Val Phe Met Gly Ala Ile Ser Asp Asp Tyr Ala Ala
            115             120             125.

ctg ctg cgc gag agc ccg ccg gaa gtg gct gcg cag tac cgc ctc acc      432
Leu Leu Arg Glu Ser Pro Pro Glu Val Ala Ala Gln Tyr Arg Leu Thr
        130             135             140

ggc acc cat cga agc ctg atc gcc aac cgc gtg tcc tat gtg ctc ggc      480
Gly Thr His Arg Ser Leu Ile Ala Asn Arg Val Ser Tyr Val.Leu Gly
145             150             155             160

ctg cgc ggg cca agc ctg acg gtg gat tca ggt cag tcc tcg tcc ctg      528
Leu Arg Gly Pro Ser Leu Thr Val Asp Ser Gly Gln Ser Ser Ser Leu
                165         .       170             175

gtc ggc gtg cat ctc gcc agc gag agc ctg cga cgg ggt gag tgc acg      576
Val Gly Val His Leu Ala Ser Glu Ser Leu Arg Arg Gly Glu Cys Thr
            180             185             190

atc gca ctc gcc ggc ggc gtg aac ctc aac ctg gcc gcc gag agc aac      624
Ile Ala Leu Ala Gly Gly Val Asn Leu Asn Leu Ala Ala Glu Ser Asn
        195             200             205

agc gct ctg atg gac ttc ggc gcg ctc tcc ccg gac ggt cgc tgc ttc      672
Ser Ala Leu Met Asp Phe Gly Ala Leu Ser Pro Asp Gly Arg Cys Phe
    210             215             220

acc ttc gat gtg cgg gcg aac ggt tac gtc cgt ggt gag ggc ggc ggc      720
Thr Phe Asp Val Arg Ala Asn Gly Tyr Val Arg Gly Glu Gly Gly Gly
225             230             235             240

ctt gtc gtg ctg aag aag gcc gat cag gcg cac gcc gat ggc gac cgg      768
Leu Val Val Leu Lys Lys Ala Asp Gln Ala His Ala Asp Gly Asp Arg
            245             250             255

atc tac tgc ctc atc cgc ggc agc gcg gtc aac aac gat ggg ggc ggt      816
Ile Tyr Cys Leu Ile Arg Gly Ser Ala Val Asn Asn Asp Gly Gly Gly
            260             265             270

gcc ggg ctc acc gtt ccg gcg gcg gac gcc cag gcg gag ctg ctg cgc      864
Ala Gly Leu Thr Val Pro Ala Ala Asp Ala Gln Ala Glu Leu Leu Arg
        275             280             285
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cag gca tac cgg aac gcg ggc gtc gac ccg gcc gcc gtg cag tat gtc    912
Gln Ala Tyr Arg Asn Ala Gly Val Asp Pro Ala Ala Val Gln Tyr Val
    290             295             300

gag ctc cac ggc agc gcg acc agg gtc ggg gat ccc gtc gaa gca gca    960
Glu Leu His Gly Ser Ala Thr Arg Val Gly Asp Pro Val Glu Ala Ala
305             310             315             320

gcc ctc gga gct gtc ctg ggg gcg gcg aga cgg ccc ggc gac gag ctg    1008
Ala Leu Gly Ala Val Leu Gly Ala Ala Arg Arg Pro Gly Asp Glu Leu
                325             330             335

cgt gtg ggg tcg gcg aag acc aac gtc ggc cat ctg gaa gca gcg gcg    1056
Arg Val Gly Ser Ala Lys Thr Asn Val Gly His Leu Glu Ala Ala Ala
                340             345             350

ggc gtc acc ggg ttg ctg aag acc gca ctc agc atc tgg cac cgc gaa    1104
Gly Val Thr Gly Leu Leu Lys Thr Ala Leu Ser Ile Trp His Arg Glu
            355             360             365

ctg ccg ccg agt ctt cat ttc acc gcc ccc aac ccg gaa atc ccg ctg    1152
Leu Pro Pro Ser Leu His Phe Thr Ala Pro Asn Pro Glu Ile Pro Leu
    370             375             380

gac gaa ttg aac cta cgc gtc cag cgt gat ctg cgg ccg tgg ccg gag    1200
Asp Glu Leu Asn Leu Arg Val Gln Arg Asp Leu Arg Pro Trp Pro Glu
385             390             395             400

agc gag ggg ccg ctg ctg gcc ggc gtc agc gcc ttc gga atg gga ggc    1248
Ser Glu Gly Pro Leu Leu Ala Gly Val Ser Ala Phe Gly Met Gly Gly
            405             410             415

acg aac tgc cac ctg gtg ctc tcc ggc acg tcc cgg gtg gag cga cgg    1296
Thr Asn Cys His Leu Val Leu Ser Gly Thr Ser Arg Val Glu Arg Arg
            420             425             430

cgc agt gga ccc gct gag gcg acc atg ccg tgg gtc ttg tcg gcc aga    1344
Arg Ser Gly Pro Ala Glu Ala Thr Met Pro Trp Val Leu Ser Ala Arg
            435             440             445

aca ccg gtc gca ttg cgt gcg cag gcg gcg cgc ttg cac acg cac ctc    1392
Thr Pro Val Ala Leu Arg Ala Gln Ala Ala Arg Leu His Thr His Leu
    450             455             460

aat acg gcc ggt caa agt ccg ttg gac gtc gcc tac tca ctg gcg acc    1440
Asn Thr Ala Gly Gln Ser Pro Leu Asp Val Ala Tyr Ser Leu Ala Thr
465             470             475             480
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act cga tcc gcg ctg ccg cac cgg gcc gcg ctg gtc gcg gac gac gaa   1488
Thr Arg Ser Ala Leu Pro His Arg Ala Ala Leu Val Ala Asp Asp Glu
            485   490   495

ccg aaa ctg ctc gcc ggg ttg aag gcc ctc gct gac ggc gac gac gcg   1536
Pro Lys Leu Leu Ala Gly Leu Lys Ala Leu Ala Asp Gly Asp Asp Ala
            500   .   505   510

ccc acg ctg tgc cac ggc gcg act tcc ggc gag cgg gca gcg gtc ttc   1584
Pro Thr Leu Cys His Gly Ala Thr Ser Gly Glu Arg Ala Ala Val Phe
            515   520   525

gtc ttt ccc gga cag ggc agc cag tgg atc ggg atg ggt agg cag ctg   1632
Val Phe Pro Gly Gln Gly Ser Gln Trp Ile Gly Met Gly Arg Gln Leu
            530   535.   540

ctc gaa acc tcc gag gtt ttc gcg gcg tcg atg tcg gac tgc gcc gac   1680
Leu Glu Thr Ser Glu Val Phe Ala Ala Ser Met Ser Asp Cys Ala Asp
545   550   555   560

gca ttg gcg ccg cac ctg gat tgg tcc ctg ctg gat gtg ctg cgc aac   1728
Ala Leu Ala Pro His Leu Asp Trp Ser Leu Leu Asp Val Leu Arg Asn
            565   570   575

gcg gcc ggc gct gcg cac ctt gac cac gac gat gtc gtc cag ccc gcg   1776
Ala Ala Gly Ala Ala His Leu Asp His Asp Asp Val Val Gln Pro Ala
            580   585 .   590

ctg ttc gcc atc atg gtc tcg ctc gcg gag ctc tgg cgt tcg tgg ggc   1824
Leu Phe Ala Ile Met Val Ser Leu Ala Glu Leu Trp Arg Ser Trp Gly
            595   600   605

gtg cgt ccg gtg gcg gtc gtc ggg cac tcg cag ggg gag atc gcg gcg   1872
Val Arg Pro Val Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala
            610   615   620

gcc tgc gtc gcc ggg gcc ctg tcc gtc cgc gat gcc gcc agg gtg gtg   1920
Ala Cys Val Ala Gly Ala Leu Ser Val Arg Asp Ala Ala Arg Val Val
625   630   635   640

gcg gtg cgc agc agg ctt ctg acg gcg ctg gcc ggc agt ggc gcg atg   1968
Ala Val Arg Ser Arg Leu Leu Thr Ala Leu Ala Gly Ser Gly Ala Met
            645   650   655

gcc tcg ttg cag cat ccc gcc gaa gag gtg cgg caa atc ctg ttg ccc   2016
Ala Ser Leu Gln His Pro Ala Glu Glu Val Arg Gln Ile Leu Leu Pro
            660   665   670

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tgg cgc gat cgg atc ggc gtg gcg ggg gtg aac gga ccg tcg tcg acc    2064
Trp Arg Asp Arg Ile Gly Val Ala Gly Val Asn Gly Pro Ser Ser Thr
        675             680             685

ctg gtg tca ggg gac cgg gag gcg atg gcg gaa ctg ctg gcc gag tgc    2112
Leu Val Ser Gly Asp Arg Glu Ala Met Ala Glu Leu Leu Ala Glu Cys
        690             695             700

gca gac cga gag ctc cgg atg cgc cgg att ccc gtt gaa tac gcc tcc    2160
Ala Asp Arg Glu Leu Arg Met Arg Arg Ile Pro Val Glu Tyr Ala Ser
705             710             715             720

cat tcg cct cac atc gag gtt gtc cgg gat gag ctg ctg ggg ctg ttg    2208
His Ser Pro His Ile Glu Val Val Arg Asp Glu Leu Leu Gly Leu Leu
            725             730             735

gcg ccg gtc gaa ccc agg acg gga agc atc ccg atc tat tcg acg acg    2256
Ala Pro Val Glu Pro Arg Thr Gly Ser Ile Pro Ile Tyr Ser Thr Thr
            740             745             750

acc ggg gac ctg ctg gac cgg ccg atg gac gcc gac tac tgg tac cgc    2304
Thr Gly Asp Leu Leu Asp Arg Pro Met Asp Ala Asp Tyr Trp Tyr Arg
            755             760             765

aac ctt cgt caa ccg gtg ctg ttc gaa gcg gcc gtc gag gcc ctg ttg    2352
Asn Leu Arg Gln Pro Val Leu Phe Glu Ala Ala Val Glu Ala Leu Leu
        770             775             780

aag cgg ggg tac gac gca ttc atc gag atc agc cca cac ccg gtg ctg    2400
Lys Arg Gly Tyr Asp Ala Phe Ile Glu Ile Ser Pro His Pro Val Leu
785             790             795             800

act gcg aac atc cag gaa acc gcc gtg cga gca ggg cgg gag gta gtg    2448
Thr Ala Asn Ile Gln Glu Thr Ala Val Arg Ala Gly Arg Glu Val Val
            805             810             815

gcg ctc ggg aca ctc cgc cgc ggc gaa ggt ggc atg cgg cag gcg ctg    2496
Ala Leu Gly Thr Leu Arg Arg Gly Glu Gly Gly Met Arg Gln Ala Leu
            820             825             830

acg tcg ctg gcc aga gca cac gta cac gga gtg gcc gcg gac tgg cac    2544
Thr Ser Leu Ala Arg Ala His Val His Gly Val Ala Ala Asp Trp His
            835             840             845

gcg gtc ttc gcc ggt acc ggg gcg cag cgg gtc gac ctg ccg acg tac    2592
Ala Val Phe Ala Gly Thr Gly Ala Gln Arg Val Asp Leu Pro Thr Tyr
        850             855             860
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gcc ttt cag cga cag cgc tac tgg ctg gac gcg aag ctt ccc gac gtc    2640
Ala Phe Gln Arg Gln Arg Tyr Trp Leu Asp Ala Lys Leu Pro Asp Val
865                 870             875             880

gcc atg ccc gag agc gac gtg tcg acg gcg ttg cgg gaa aag ctg cgg    2688
Ala Met Pro Glu Ser Asp Val Ser Thr Ala Leu Arg Glu Lys Leu Arg
                885             890             895

tct tcg ccg agg gcg gac gtg gac tcg acg acc ctc acg atg atc cgg    2736
Ser Ser Pro Arg Ala Asp Val Asp Ser Thr Thr Leu Thr Met Ile Arg
                900             905             910

gca cag gca gcc gtg gtc ctc ggc cac tcc gat ccg aaa gag gtg gac    2784
Ala Gln Ala Ala Val Val Leu Gly His Ser Asp Pro Lys Glu Val Asp
        915             920             925

ccg gat cgg acg ttc aag gac ctg ggc ttc gat tcc tcg atg gtg gtc    2832
Pro Asp Arg Thr Phe Lys Asp Leu Gly Phe Asp Ser Ser Met Val Val
        930             935             940

gag ctg tgc gac cgc cta aac gcc gcc aca ggt ctg cga ctc gca ccg    2880
Glu Leu Cys Asp Arg Leu Asn Ala Ala Thr Gly Leu Arg Leu Ala Pro
945             950             955             960

agc gtc gtt ttc gac tgt cct acg ccg gac aag ctc gcc cgc cag gta    2928
Ser Val Val Phe Asp Cys Pro Thr Pro Asp Lys Leu Ala Arg Gln Val
                965             970             975

cgg acg ttg ttg ttg ggc gag ccg gct ccc atg acg tca cac cgg ccg    2976
Arg Thr Leu Leu Leu Gly Glu Pro Ala Pro Met Thr Ser His Arg Pro
                980             985             990

gac tcc gat gcg gac gag cct atc gcc gtg atc ggg atg ggc tgt cgg    3024
Asp Ser Asp Ala Asp Glu Pro Ile Ala Val Ile Gly Met Gly Cys Arg
        995             1000            1005

ttt ccg ggt ggg gtg tcc tcg ccc gag gag ttg tgg cag ttg gtc gcc    3072
Phe Pro Gly Gly Val Ser Ser Pro Glu Glu Leu Trp Gln Leu Val Ala
    1010            1015            1020

gct ggg cgg gac gtc gtg tcc gag ttc ccg gct gac cga ggt tgg gac    3120
Ala Gly Arg Asp Val Val Ser Glu Phe Pro Ala Asp Arg Gly Trp Asp
1025            1030            1035            1040

ctg gag cgt gcg ggg aca tcg cac gtg cgc gcc ggc ggg ttc ttg cat    3168
Leu Glu Arg Ala Gly Thr Ser His Val Arg Ala Gly Gly Phe Leu His
                1045            1050            1055
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ggc gcc ccg gat ttt gac ccc ggg ttc ttc cgg att tcg ccg cgc gag   3216
Gly Ala Pro Asp Phe Asp Pro Gly Phe Phe Arg Ile Ser Pro Arg Glu
         1060   1065   1070

gcg ttg gcg atg gat cca cag cag cgg ttg ctg ctg gaa atc gcc tgg   3264
Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Ile Ala Trp
         1075   1080   1085

gaa gca gtc gaa cga ggc ggg atc aac ccg cag cac ctg cac gga agt   3312
Glu Ala Val Glu Arg Gly Gly Ile Asn Pro Gln His Leu His Gly Ser
         1090   1095   1100

caa acc ggg gtc ttc gtc ggc gcg acc tcc ctg gac tac ggg cca cgc   3360
Gln Thr Gly Val Phe Val Gly Ala Thr Ser Leu Asp Tyr Gly Pro Arg
1105   1110   1115   1120

ctg cac gaa gcg tcc gag gag gcg gcc ggg tac gtg ctc acc ggc agc   3408
Leu His Glu Ala Ser Glu Glu Ala Ala Gly Tyr Val Leu Thr Gly Ser
              1125   1130   1135

acc acg agt gtg gcg tcg ggt cgg gtt gcg tat tcg ttc ggg ttc gag   3456
Thr Thr Ser Val Ala Ser Gly Arg Val Ala Tyr Ser Phe Gly Phe Glu
         1140   1145   1150

ggc cct gcg gtg acg gtg gat acg gcg tgt tcg tcg tcg ttg gtg gcc   3504
Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala
         1155   1160   1165

ctg cat ttg gcg tgt cag tcg ttg cgt tcg ggt gag tgt gat ctg gcg   3552
Leu His Leu Ala Cys Gln Ser Leu Arg Ser Gly Glu Cys Asp Leu Ala
         1170   1175   1180

ttg gcc ggt ggt gtg acc gtg atg gcc acg ccg ggg atg ttc gtg gag   3600
Leu Ala Gly Gly Val Thr Val Met Ala Thr Pro Gly Met Phe Val Glu
1185   1190   1195   1200

ttt tcg cgg cag cgt ggt ttg gcg ccg gat ggg cgg tgc aag tcg ttc   3648
Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Lys Ser Phe
              1205   1210   1215

gcg gag gcc gcc gac ggc acc ggc tgg tcc gag ggt gct ggc ctg gtt   3696
Ala Glu Ala Ala Asp Gly Thr Gly Trp Ser Glu Gly Ala Gly Leu Val
              1220   1225   1230

cta ctg gag cgg ttg tcg gat gcc cgg cgg aat ggg cat gag gtg ctg   3744
Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly His Glu Val Leu
         1235   1240   1245

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gcg gtt gtt cgt ggt agt gcg gtg aat cag gac ggt gcg tcg aat ggt    3792
Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly
   1250            1255            1260


ttg acc gcg ccg aat ggt tcg tcg cag cag cgg gtg att gcc cag gca    3840
Leu Thr Ala Pro Asn Gly Ser Ser Gln Gln Arg Val Ile Ala Gln Ala
   1265            1270            1275            1280


ttg gcg agt gcg ggg ttg tcg gtg tcc gat gtg gat gct gtg gag gcg    3888
Leu Ala Ser Ala Gly Leu Ser Val Ser Asp Val Asp Ala Val Glu Ala
            1285            1290            1295


cat ggg acg ggc acg cgg ctt ggt gat ccg atc gag gcg cag gcg ctg    3936
His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu
            1300            1305            1310


atc gcc acc tac ggc cag ggc cgg ctt ccg gaa cgg cca ttg tgg ttg    3984
Ile Ala Thr Tyr Gly Gln Gly Arg Leu Pro Glu Arg Pro Leu Trp Leu
            1315            1320            1325


ggc tcg atg aag tcg aac atc ggt cac gcg cag gca gct gcg ggg ata    4032
Gly Ser Met Lys Ser Asn Ile Gly His Ala Gln Ala Ala Ala Gly Ile
            1330            1335            1340


gcc ggc gtc atg aag atg gtg atg gcg atg cgg cac ggg cag cta ccg    4080
Ala Gly Val Met Lys Met Val Met Ala Met Arg His Gly Gln Leu Pro
   1345            1350            1355            1360


cgc acg ttg cac gtg gat gag ccg act tct ggg gtg gat tgg tcg gcg    4128
Arg Thr Leu His Val Asp Glu Pro Thr Ser Gly Val Asp Trp Ser Ala
            1365            1370            1375


ggg acg gtt caa ctc ctt acg gag aac acg ccc tgg ccc ggg agt ggt    4176
Gly Thr Val Gln Leu Leu Thr Glu Asn Thr Pro Trp Pro Gly Ser Gly
            1380            1385            1390


cgt gtt cgt cgg gtg ggg gtg tcg tcg ttc ggg atc agt ggt act aac    4224
Arg Val Arg Arg Val Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn
   1395            1400            1405


gcg cac gtc atc ctc gaa cag ccc ccg gga gtg ccg agt cag tct gcg    4272
Ala His Val Ile Leu Glu Gln Pro Pro Gly Val Pro Ser Gln Ser Ala
   1410            1415            1420


ggg ccg ggt tcg ggc tct gtc gtg gat gtt ccg gtg gtg ccg tgg atg    4320
Gly Pro Gly Ser Gly Ser Val Val Asp Val Pro Val Val Pro Trp Met
1425            1430            1435            1440
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gtg tcg ggc aaa aca ccc gaa gcg cta tcc gcg cag gca acg gcg ttg      4368
Val Ser Gly Lys Thr Pro Glu Ala Leu Ser Ala Gln Ala Thr Ala Leu
            1445              1450              1455

atg acc tat ctg gac gag cga cct gat gtc tcc tcg ctg gat gtt ggg      4416
Met Thr Tyr Leu Asp Glu Arg Pro Asp Val Ser Ser Leu Asp Val Gly
            1460              1465              1470

tac tcg ctg gcg ttg aca cgg tcg gcg ctg gat gag cga gcg gtg gtg      4464
Tyr Ser Leu Ala Leu Thr Arg Ser Ala Leu Asp Glu Arg Ala Val Val
        1475              1480              1485

ctg ggg tcg gac cgt gaa acg ttg ttg tgc ggt gtg aaa gcg ctg tct      4512
Leu Gly Ser Asp Arg Glu Thr Leu Leu Cys Gly Val Lys Ala Leu Ser
      1490              1495              1500

gcc ggt cat gag gct tct ggg ttg gtg acc gga tct gtg ggg gct ggg      4560
Ala Gly His Glu Ala Ser Gly Leu Val Thr Gly Ser Val Gly Ala Gly
1505              1510              1515              1520

ggc cgc atc ggg ttt gtg ttt tcc ggt cag ggt ggt cag tgg ctg ggg      4608
Gly Arg Ile Gly Phe Val Phe Ser Gly Gln Gly Gly Gln Trp Leu Gly
            1525              1530              1535

atg ggc cgg ggg ctt tac cgg gct ttt ccg gtg ttc gct gct gcc ttt      4656
Met Gly Arg Gly Leu Tyr Arg Ala Phe Pro Val Phe Ala Ala Ala Phe
            1540              1545              1550

gac gaa gct tgt gcc gag ctg gat gcg cat ctg ggc cag gaa atc ggg      4704
Asp Glu Ala Cys Ala Glu Leu Asp Ala His Leu Gly Gln Glu Ile Gly
            1555              1560              1565

gtt cgg gag gtg gtg tcc ggt tcg gat gcg cag ttg ctg gat cgg acg      4752
Val Arg Glu Val Val Ser Gly Ser Asp Ala Gln Leu Leu Asp Arg Thr
      1570              1575              1580

ttg tgg gcg cag tcg ggt ttg ttc gcg ttg cag gtg ggc ttg ctg aag      4800
Leu Trp Ala Gln Ser Gly Leu Phe Ala Leu Gln Val Gly Leu Leu Lys
1585              1590              1595              1600

ttg ctg gat tcg tgg ggg gtt cgg ccg agt gtg gtg ttg ggg cat tcg      4848
Leu Leu Asp Ser Trp Gly Val Arg Pro Ser Val Val Leu Gly His Ser
            1605              1610              1615

gtg ggc gag ttg gcg gcg gcg ttc gcg gcg ggt gtg gtg tcg ttg tcg      4896
Val Gly Glu Leu Ala Ala Ala Phe Ala Ala Gly Val Val Ser Leu Ser
            1620              1625              1630
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160

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ggt gcg gct cgg ttg gtg gcg ggt cgt gcc cgg ttg atg cag gcg ttg    4944
Gly Ala Ala Arg Leu Val Ala Gly Arg Ala Arg Leu Met Gln Ala Leu
      1635              1640          1645

ccg tct ggc ggt ggg atg ctg gcg gtg cct gct ggt gag gag ctg ttg    4992
Pro Ser Gly Gly Gly Met Leu Ala Val Pro Ala Gly Glu Glu Leu Leu
      1650          1655          1660

tgg tcg ttg ttg gcc gat cag ggt gat cgt gtg ggg atc gcc gcg gtc    5040
Trp Ser Leu Leu Ala Asp Gln Gly Asp Arg Val Gly Ile Ala Ala Val
  1665          1670          1675          1680

aac gct gcg ggg tcg gtg gtg ctc tct ggt gat cgg gat gtg ctc gat    5088
Asn Ala Ala Gly Ser Val Val Leu Ser Gly Asp Arg Asp Val Leu Asp
          1685          1690          1695

gac ctt gcc ggt cgg ctg gac ggg caa ggg atc cgg tcg agg tgg ttg    5136
Asp Leu Ala Gly Arg Leu Asp Gly Gln Gly Ile Arg Ser Arg Trp Leu
          1700          1705          1710

cgg gtg tcg cat gcg ttt cat tcg tat cgg atg gat ccg atg ctg gcg    5184
Arg Val Ser His Ala Phe His Ser Tyr Arg Met Asp Pro Met Leu Ala
          1715          1720          1725

gag ttc gcc gaa ttg gca cga acc gtg gat tac cgg cgt tgt gaa gtg    5232
Glu Phe Ala Glu Leu Ala Arg Thr Val Asp Tyr Arg Arg Cys Glu Val
      1730          1735          1740

ccg atc gtg tcg acc ttg acc gga gac ctc gat gac gct ggc agg atg    5280
Pro Ile Val Ser Thr Leu Thr Gly Asp Leu Asp Asp Ala Gly Arg Met
1745          1750          1755          1760

agc ggg ccc gac tac tgg gtg cgt cag gtg cga gag ccg gtc cgc ttc    5328
Ser Gly Pro Asp Tyr Trp Val Arg Gln Val Arg Glu Pro Val Arg Phe
          1765          1770          1775

gcc gac ggt gtc cag gcg ctg gtc gag cac gat gtg gcc acc gtt gtc    5376
Ala Asp Gly Val Gln Ala Leu Val Glu His Asp Val Ala Thr Val Val
          1780          1785          1790

gag ctc ggt ccg gac ggg gcg ttg tcg gcg ctg atc cag gaa tgt gtc    5424
Glu Leu Gly Pro Asp Gly Ala Leu Ser Ala Leu Ile Gln Glu Cys Val
      1795          1800          1805

gcc gca tcc gat cac gcc ggg cgg ctg agc gcg gtc ccg gcg atg cgc    5472
Ala Ala Ser Asp His Ala Gly Arg Leu Ser Ala Val Pro Ala Met Arg
  1810          1815          1820
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161

agg aac cag gac gag gcg cag aag gtg atg acg gcc ctg gca cac gtc   5520
Arg Asn Gln Asp Glu Ala Gln Lys Val Met Thr Ala Leu Ala His Val
1825   1830   1835   1840

cac gta cgt ggt ggt gcg gtg gac tgg cgg tcg ttc ttc gcc ggt aca   5568
His Val Arg Gly Gly Ala Val Asp Trp Arg Ser Phe Phe Ala Gly Thr
                    1845   1850   1855

agg gcg aag caa atc gag ctg ccc acc tac gcc ttc caa cga cag cgg   5616
Arg Ala Lys Gln Ile Glu Leu Pro Thr Tyr Ala Phe Gln Arg Gln Arg
                1860   1865   1870

tac tgg ctg aac gcg ctg cgt gaa tct tcc gcc ggc gac atg ggc agg   5664
Tyr Trp Leu Asn Ala Leu Arg Glu Ser Ser Ala Gly Asp Met Gly Arg
                1875   1880   1885

cgt gtc gaa gcg aag ttc tgg ggc gcc gtc gag cac gaa gat gtg gaa   5712
Arg Val Glu Ala Lys Phe Trp Gly Ala Val Glu His Glu Asp Val Glu
            1890   1895   1900

tcg ctt gca cgc gta ttg ggc att gtg gac gac ggc gct gct gtg gat   5760
Ser Leu Ala Arg Val Leu Gly Ile Val Asp Asp Gly Ala Ala Val Asp
1905   1910   1915   1920

tcc ctg aga agc gcc ctt ccg gtg ttg gcc ggt tgg cag cga acc cgc   5808
Ser Leu Arg Ser Ala Leu Pro Val Leu Ala Gly Trp Gln Arg Thr Arg
                1925   1930   1935

acc acc gag tcc att atg gat cag cgg tgt tac cga att ggc tgg cgg   5856
Thr Thr Glu Ser Ile Met Asp Gln Arg Cys Tyr Arg Ile Gly Trp Arg
                1940   1945   1950

cag gta gcc gga ctc ccg ccg atg gga act gtt ttc ggt acc tgg ctg   5904
Gln Val Ala Gly Leu Pro Pro Met Gly Thr Val Phe Gly Thr Trp Leu
            1955   1960   1965

gtc ttc gcg cct cat ggc tgg tcc agc gaa ccg gag gtg gtg gac tgc   5952
Val Phe Ala Pro His Gly Trp Ser Ser Glu Pro Glu Val Val Asp Cys
            1970   1975   1980

gtt acg gca ctg cgg gca cgt ggt gcc tcg gtg gtg ttg gtg gaa gct   6000
Val Thr Ala Leu Arg Ala Arg Gly Ala Ser Val Val Leu Val Glu Ala
1985   1990   1995   2000

gat ccc gac ccg acc tcc ttc ggc gac cgg gta cga acc ctg tgt tcg   6048
Asp Pro Asp Pro Thr Ser Phe Gly Asp Arg Val Arg Thr Leu Cys Ser
                2005   2010   2015

162

ggc ctt ccg gat ctt gtt ggc gtg ttg tca atg ttg tgc ttg gaa gaa   6096
Gly Leu Pro Asp Leu Val Gly Val Leu Ser Met Leu Cys Leu Glu Glu
           2020   2025   2030

tcg gtc ctt ccg gga ttt tct gcg gtg tca cgg ggt ttt gcg ttg acc   6144
Ser Val Leu Pro Gly Phe Ser Ala Val Ser Arg Gly Phe Ala Leu Thr
        2035   2040   2045

gtg gag ttg gtg cgg gtt ttg cgg gca gct ggt gcg act gcc cgg ttg   6192
Val Glu Leu Val Arg Val Leu Arg Ala Ala Gly Ala Thr Ala Arg Leu
     2050   2055   2060

tgg ttg ctg acg tgt ggt ggc gtg tcg gtg gga gat gta ccg gtt cgt   6240
Trp Leu Leu Thr Cys Gly Gly Val Ser Val Gly Asp Val Pro Val Arg
2065   2070   2075   2080

cca gcg cag gcc ctg gcg tgg ggg ttg ggg cgt gtt gtg ggg ttg gag   6288
Pro Ala Gln Ala Leu Ala Trp Gly Leu Gly Arg Val Val Gly Leu Glu
                2085   2090   2095

cat ccg gac tgg tgg ggc ggc ttg atc gat att ccg gtc ttg ttc gac   6336
His Pro Asp Trp Trp Gly Gly Leu Ile Asp Ile Pro Val Leu Phe Asp
           2100   2105   2110

gaa gac gct caa gag cgg ttg tcg att gtg ctg gca ggt ctc gat gag   6384
Glu Asp Ala Gln Glu Arg Leu Ser Ile Val Leu Ala Gly Leu Asp Glu
        2115   2120   2125

gac gag gtc gcg atc cgt cct gac ggc atg ttc gcg cgt cgg ttg gta   6432
Asp Glu Val Ala Ile Arg Pro Asp Gly Met Phe Ala Arg Arg Leu Val
     2130   2135   2140

cgc cac act gtc tca gct gat gtg aag aag gcg tgg cgc ccc agg gga   6480
Arg His Thr Val Ser Ala Asp Val Lys Lys Ala Trp Arg Pro Arg Gly
2145   2150   2155   2160

tcg gtg ctg gtg acg ggc ggc acg ggt ggt ttg ggg gcg cac gtt gct   6528
Ser Val Leu Val Thr Gly Gly Thr Gly Gly Leu Gly Ala His Val Ala
                2165   2170   2175

cgc tgg ctg gcc gac gcc gga gcc gaa cat gtg gcg atg gtg agt cga   6576
Arg Trp Leu Ala Asp Ala Gly Ala Glu His Val Ala Met Val Ser Arg
           2180   2185   2190

cgc ggc gag cag gca ccg agt gct gag aag ttg cgg acg gaa ctg gag   6624
Arg Gly Glu Gln Ala Pro Ser Ala Glu Lys Leu Arg Thr Glu Leu Glu
        2195   2200   2205

163

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gat ctg ggt acc cgg gtg tcg atc gtg tca tgc gat gtg acc gat cgc    6672
Asp Leu Gly Thr Arg Val Ser Ile Val Ser Cys Asp Val Thr Asp Arg
    2210               2215               2220

gag gcg ctc gcc gaa gtg ctg aaa gcc ctt ccg gct gaa aac ccg ttg    6720
Glu Ala Leu Ala Glu Val Leu Lys Ala Leu Pro Ala Glu Asn Pro Leu
    2225               2230               2235               2240

acc gcg gta gtg cat gcg gca ggc gtg atc gag act ggt gat gcg gcg    6768
Thr Ala Val Val His Ala Ala Gly Val Ile Glu Thr Gly Asp Ala Ala
                2245               2250               2255

gca atg agc ctg gct gat ttc gat cac gtg ttg tcc gca aag gtg gcc    6816
Ala Met Ser Leu Ala Asp Phe Asp His Val Leu Ser Ala Lys Val Ala
                2260               2265               2270

ggt gcc gcg aat ctg gat gcc ttg ttg gcc gat gtg gaa ttg gac gcg    6864
Gly Ala Ala Asn Leu Asp Ala Leu Leu Ala Asp Val Glu Leu Asp Ala
                2275               2280               2285

ttc gtc ttg ttc tca tcg gtg tca gga gtt tgg ggc gct ggg gga cac    6912
Phe Val Leu Phe Ser Ser Val Ser Gly Val Trp Gly Ala Gly Gly His
    2290               2295                    2300

ggg gct tac gca gcg gcg aat gcc tat ctg gat gcg ctc gcg gaa cag    6960
Gly Ala Tyr Ala Ala Ala Asn Ala Tyr Leu Asp Ala Leu Ala Glu Gln
2305               2310               2315               2320

cgt cgg tcg cga ggg ctg gtc gcg act gcg gtg gcc tgg ggg ccg tgg    7008
Arg Arg Ser Arg Gly Leu Val Ala Thr Ala Val Ala Trp Gly Pro Trp
                2325               2330               2335

gcc ggc gag ggc atg gcc tcc gga gaa aca gga gac cag ctg cgc cga    7056
Ala Gly Glu Gly Met Ala Ser Gly Glu Thr Gly Asp Gln Leu Arg Arg
                2340               2345               2350

tac ggc ctt tcc cca atg gct ccg cag cac gcc atc gcc gga atc cgg    7104
Tyr Gly Leu Ser Pro Met Ala Pro Gln His Ala Ile Ala Gly Ile Arg
                2355               2360               2365

cag gcc gtg gaa cag gac gaa att tcc ctg gta gtg gcc gat gtc gat    7152
Gln Ala Val Glu Gln Asp Glu Ile Ser Leu Val Val Ala Asp Val Asp
    2370               2375               2380

tgg gca cgt ttc agc gcg gga ttg ctg gcg gct agg ccg cgg ccg ctg    7200
Trp Ala Arg Phe Ser Ala Gly Leu Leu Ala Ala Arg Pro Arg Pro Leu
    2385               2390               2395               2400
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164

ctg aac gaa ctg gcc gag gtc aag gaa ctc ctc gtc gat gcc cag ccc   7248
Leu Asn Glu Leu Ala Glu Val Lys Glu Leu Leu Val Asp Ala Gln Pro
            2405   2410   2415

gag gcg gga gtc ctt gcc gac gcg tcg ttg gaa tgg cgg cag cga ttg   7296
Glu Ala Gly Val Leu Ala Asp Ala Ser Leu Glu Trp Arg Gln Arg Leu
            2420   2425   2430

tcc gcg gca ccg agg ccg aca cag gaa cag ctg atc ctg gag ctg gta   7344
Ser Ala Ala Pro Arg Pro Thr Gln Glu Gln Leu Ile Leu Glu Leu Val
            2435   2440   2445

cgc ggc gaa acc gct ctg gtg ctg gga cac ccc ggg gca gcg gcc gtt   7392
Arg Gly Glu Thr Ala Leu Val Leu Gly His Pro Gly Ala Ala Ala Val
            2450   2455   2460

gca tcg gaa cga gcc ttc aag gac agc gga ttc gac tcg cag gcc gcg   7440
Ala Ser Glu Arg Ala Phe Lys Asp Ser Gly Phe Asp Ser Gln Ala Ala
2465   2470   2475   2480

gtc gaa ctc cgc gtt cgg ctc aat cga gct acc ggc ctc cag ttg cca   7488
Val Glu Leu Arg Val Arg Leu Asn Arg Ala Thr Gly Leu Gln Leu Pro
            2485   2490   2495

tcg aca att atc ttc agc cat ccc acg cct gcg gaa ctg gct gcg gag   7536
Ser Thr Ile Ile Phe Ser His Pro Thr Pro Ala Glu Leu Ala Ala Glu
            2500   2505   2510

ctg cgg gcg agg ctt ctt ccc gag tcc gca gga gca ggc att ccc gag   7584
Leu Arg Ala Arg Leu Leu Pro Glu Ser Ala Gly Ala Gly Ile Pro Glu
            2515   2520   2525

gag gac gag gcg cga atc aga gcg gca ctg acg tcg atc ccg ttc ccg   7632
Glu Asp Glu Ala Arg Ile Arg Ala Ala Leu Thr Ser Ile Pro Phe Pro
    2530   2535   2540

gcc ttg cgc gag gca ggc ttg gtg agt ccg ctg ctc gca ctt gcc gga   7680
Ala Leu Arg Glu Ala Gly Leu Val Ser Pro Leu Leu Ala Leu Ala Gly
2545   2550   2555   2560

cac ccg gtc gac tcc ggt atc tcc tcg gac gat gcg gcc gcg acc tcg   7728
His Pro Val Asp Ser Gly Ile Ser Ser Asp Asp Ala Ala Ala Thr Ser
            2565   2570   2575

atc gat gcg atg gat gta gcc ggc ctc gtc gaa gca gcg ctg ggc gaa   7776
Ile Asp Ala Met Asp Val Ala Gly Leu Val Glu Ala Ala Leu Gly Glu
            2580   2585   2590

165

cgc gag tcc tga   7788
Arg Glu Ser
        2595

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<213> Saccharopolyspora spinosa

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Met Ser Glu Ala Gly Asn Leu Ile Ala Val Ile Gly Leu Ser Cys Arg
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Leu Pro Gln Ala Pro Asp Pro Ala Ser Phe Trp Arg Leu Leu Arg Thr
            20   25   30

Gly Thr Asp Ala Ile Thr Thr Val Pro Glu Gly Arg Trp Gly Asp Pro
          35   40   45

Leu Pro Gly Arg Asp Ala Pro Lys Gly Pro Glu Trp Gly Gly Phe Leu
      50   55   60

Ala Asp Val Asp Cys Phe Asp Pro Glu Phe Phe Gly Ile Ser Pro Arg
 65   70   75   80

Glu Ala Ala Ala Val Asp Pro Gln Gln Arg Leu Ala Leu Glu Leu Ala
                85   90   95

Trp Glu Ala Leu Glu Asp Ala Gly Ile Pro Ala Gly Glu Leu Arg Gly
            100   105   110

Thr Ala Ala Gly Val Phe Met Gly Ala Ile Ser Asp Asp Tyr Ala Ala
          115   120   125

Leu Leu Arg Glu Ser Pro Pro Glu Val Ala Ala Gln Tyr Arg Leu Thr
      130   135   140

Gly Thr His Arg Ser Leu Ile Ala Asn Arg Val Ser Tyr Val Leu Gly
145   150   155   160

Leu Arg Gly Pro Ser Leu Thr Val Asp Ser Gly Gln Ser Ser Ser Leu
              165   170   175

Val Gly Val His Leu Ala Ser Glu Ser Leu Arg Arg Gly Glu Cys Thr
              180   185   190

166

Ile Ala Leu Ala Gly Gly Val Asn Leu Asn Leu Ala Ala Glu Ser Asn
       195   200   205

Ser Ala Leu Met Asp Phe Gly Ala Leu Ser Pro Asp Gly Arg Cys Phe
     210   215   220

Thr Phe Asp Val Arg Ala Asn Gly Tyr Val Arg Gly Glu Gly Gly Gly
225   230   235   240

Leu Val Val Leu Lys Lys Ala Asp Gln Ala His Ala Asp Gly Asp Arg
          245   250   255

Ile Tyr Cys Leu Ile Arg Gly Ser Ala Val Asn Asn Asp Gly Gly Gly
         260   265   270

Ala Gly Leu Thr Val Pro Ala Ala Asp Ala Gln Ala Glu Leu Leu Arg
       275   280   285

Gln Ala Tyr Arg Asn Ala Gly Val Asp Pro Ala Ala Val Gln Tyr Val
     290   295   300

Glu Leu His Gly Ser Ala Thr Arg Val Gly Asp Pro Val Glu Ala Ala
305   310   315   320

Ala Leu Gly Ala Val Leu Gly Ala Ala Arg Arg Pro Gly Asp Glu Leu
         325   330   335

Arg Val Gly Ser Ala Lys Thr Asn Val Gly His Leu Glu Ala Ala Ala
         340   345   350

Gly Val Thr Gly Leu Leu Lys Thr Ala Leu Ser Ile Trp His Arg Glu
       355   360   365

Leu Pro Pro Ser Leu His Phe Thr Ala Pro Asn Pro Glu Ile Pro Leu
     370   375   380

Asp Glu Leu Asn Leu Arg Val Gln Arg Asp Leu Arg Pro Trp Pro Glu
385   390   395   400

Ser Glu Gly Pro Leu Leu Ala Gly Val Ser Ala Phe Gly Met Gly Gly
         405   410   415

Thr Asn Cys His Leu Val Leu Ser Gly Thr Ser Arg Val Glu Arg Arg
         420   425   430

Arg Ser Gly Pro Ala Glu Ala Thr Met Pro Trp Val Leu Ser Ala Arg
       435   440   445

Thr Pro Val Ala Leu Arg Ala Gln Ala Ala Arg Leu His Thr His Leu
    450   455   460

Asn Thr Ala Gly Gln Ser Pro Leu Asp Val Ala Tyr Ser Leu Ala Thr
465   470   475   480

Thr Arg Ser Ala Leu Pro His Arg Ala Ala Leu Val Ala Asp Asp Glu
                485   490   495

Pro Lys Leu Leu Ala Gly Leu Lys Ala Leu Ala Asp Gly Asp Asp Ala
            500   505   510

Pro Thr Leu Cys His Gly Ala Thr Ser Gly Glu Arg Ala Ala Val Phe
        515   520   525

Val Phe Pro Gly Gln Gly Ser Gln Trp Ile Gly Met Gly Arg Gln Leu
    530   535   540

Leu Glu Thr Ser Glu Val Phe Ala Ala Ser Met Ser Asp Cys Ala Asp
545   550   555   560

Ala Leu Ala Pro His Leu Asp Trp Ser Leu Leu Asp Val Leu Arg Asn
                565   570   575

Ala Ala Gly Ala Ala His Leu Asp His Asp Asp Val Val Gln Pro Ala
            580   585   590

Leu Phe Ala Ile Met Val Ser Leu Ala Glu Leu Trp Arg Ser Trp Gly
        595   600   605

Val Arg Pro Val Ala Val Val Gly His Ser Gln Gly Glu Ile Ala Ala
    610   615   620

Ala Cys Val Ala Gly Ala Leu Ser Val Arg Asp Ala Ala Arg Val Val
625   630   635   640

Ala Val Arg Ser Arg Leu Leu Thr Ala Leu Ala Gly Ser Gly Ala Met
                645   650   655

Ala Ser Leu Gln His Pro Ala Glu Glu Val Arg Gln Ile Leu Leu Pro
            660   665   670

Trp Arg Asp Arg Ile Gly Val Ala Gly Val Asn Gly Pro Ser Ser Thr
        675   680   685

Leu Val Ser Gly Asp Arg Glu Ala Met Ala Glu Leu Leu Ala Glu Cys
    690   695   700

168

Ala Asp Arg Glu Leu Arg Met Arg Arg Ile Pro Val Glu Tyr Ala Ser
705   710   715   720

His Ser Pro His Ile Glu Val Val Arg Asp Glu Leu Leu Gly Leu Leu
             725   730   735

Ala Pro Val Glu Pro Arg Thr Gly Ser Ile Pro Ile Tyr Ser Thr Thr
         740   745   750

Thr Gly Asp Leu Leu Asp Arg Pro Met Asp Ala Asp Tyr Trp Tyr Arg
     755   760   765

Asn Leu Arg Gln Pro Val Leu Phe Glu Ala Ala Val Glu Ala Leu Leu
     770   775   780

Lys Arg Gly Tyr Asp Ala Phe Ile Glu Ile Ser Pro His Pro Val Leu
785   790   795   800

Thr Ala Asn Ile Gln Glu Thr Ala Val Arg Ala Gly Arg Glu Val Val
             805   810   815

Ala Leu Gly Thr Leu Arg Arg Gly Glu Gly Gly Met Arg Gln Ala Leu
         820   825   830

Thr Ser Leu Ala Arg Ala His Val His Gly Val Ala Ala Asp Trp His
     835   840   845

Ala Val Phe Ala Gly Thr Gly Ala Gln Arg Val Asp Leu Pro Thr Tyr
     850   855   860

Ala Phe Gln Arg Gln Arg Tyr Trp Leu Asp Ala Lys Leu Pro Asp Val
865   870   875   880

Ala Met Pro Glu Ser Asp Val Ser Thr Ala Leu Arg Glu Lys Leu Arg
             885   890   895

Ser Ser Pro Arg Ala Asp Val Asp Ser Thr Thr Leu Thr Met Ile Arg
         900   905   910

Ala Gln Ala Ala Val Val Leu Gly His Ser Asp Pro Lys Glu Val Asp
     915   920   925

Pro Asp Arg Thr Phe Lys Asp Leu Gly Phe Asp Ser Ser Met Val Val
     930   935   940

Glu Leu Cys Asp Arg Leu Asn Ala Ala Thr Gly Leu Arg Leu Ala Pro
945   950   955   960

169

Ser Val Val Phe Asp Cys Pro Thr Pro Asp Lys Leu Ala Arg Gln Val
            965   970   975

Arg Thr Leu Leu Leu Gly Glu Pro Ala Pro Met Thr Ser His Arg Pro·
        980   985   990

Asp Ser Asp Ala Asp Glu Pro Ile Ala Val Ile Gly Met Gly Cys Arg
    995   1000   1005

Phe Pro Gly Gly Val Ser Ser Pro Glu Glu Leu Trp Gln Leu Val Ala
    1010   1015   1020

Ala Gly Arg Asp Val Val Ser Glu Phe Pro Ala Asp Arg Gly Trp Asp
025   1030   1035   1040

Leu Glu Arg Ala Gly Thr Ser His Val Arg Ala Gly Gly Phe Leu His·
        1045   1050   1055

Gly Ala Pro Asp Phe Asp Pro Gly Phe Phe Arg Ile Ser Pro Arg Glu
        1060   1065   1070

Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Ile Ala Trp
        1075   1080   1085

Glu Ala Val Glu Arg Gly Gly Ile Asn Pro Gln His Leu His Gly Ser
    1090   1095   1100

Gln Thr Gly Val Phe Val Gly Ala Thr Ser Leu Asp Tyr Gly Pro Arg
105   1110   1115   1120

Leu His Glu Ala Ser Glu Glu Ala Ala Gly Tyr Val Leu Thr Gly Ser
        1125   1130   1135

Thr Thr Ser Val Ala Ser Gly Arg Val Ala Tyr Ser Phe Gly Phe Glu
        1140   1145   1150

Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala
        1155   1160   1165

Leu His Leu Ala Cys Gln Ser Leu Arg Ser Gly Glu Cys Asp Leu Ala
    1170   1175   1180

Leu Ala Gly Gly Val Thr Val Met Ala Thr Pro Gly Met Phe Val Glu
185   1190   1195   1200

Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Lys Ser Phe
        1205   1210   1215

170

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Ala Glu Ala Ala Asp Gly Thr Gly Trp Ser Glu Gly Ala Gly Leu Val
          1220              1225              1230

Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly His Glu Val Leu
          1235              1240              1245

Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly
     1250              1255              1260

Leu Thr Ala Pro Asn Gly Ser Ser Gln Gln Arg Val Ile Ala Gln Ala
265              1270              1275              1280

Leu Ala Ser Ala Gly Leu Ser Val Ser Asp Val Asp Ala Val Glu Ala
               1285              1290              1295

His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu
          1300              1305              1310

Ile Ala Thr Tyr Gly Gln Gly Arg Leu Pro Glu Arg Pro Leu Trp Leu
     1315              1320              1325

Gly Ser Met Lys Ser Asn Ile Gly His Ala Gln Ala Ala Ala Gly Ile
     1330              1335              1340

Ala Gly Val Met Lys Met Val Met Ala Met Arg His Gly Gln Leu Pro
345              1350              1355              1360

Arg Thr Leu His Val Asp Glu Pro Thr Ser Gly Val Asp Trp Ser Ala
               1365              1370              1375

Gly Thr Val Gln Leu Leu Thr Glu Asn Thr Pro Trp Pro Gly Ser Gly
          1380              1385              1390

Arg Val Arg Arg Val Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn
     1395              1400              1405

Ala His Val Ile Leu Glu Gln Pro Pro Gly Val Pro Ser Gln Ser Ala
     1410              1415              1420

Gly Pro Gly Ser Gly Ser Val Val Asp Val Pro Val Val Pro Trp Met
425              1430              1435              1440

Val Ser Gly Lys Thr Pro Glu Ala Leu Ser Ala Gln Ala Thr Ala Leu
               1445              1450              1455

Met Thr Tyr Leu Asp Glu Arg Pro Asp Val Ser Ser Leu Asp Val Gly
          1460              1465              1470
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Tyr Ser Leu Ala Leu Thr Arg Ser Ala Leu Asp Glu Arg Ala Val Val
     1475   1480   1485

Leu Gly Ser Asp Arg Glu Thr Leu Leu Cys Gly Val Lys Ala Leu Ser
   1490   1495   1500

Ala Gly His Glu Ala Ser Gly Leu Val Thr Gly Ser Val Gly Ala Gly
505   1510   1515   1520

Gly Arg Ile Gly Phe Val Phe Ser Gly Gln Gly Gly Gln Trp Leu Gly
            1525   1530   1535

Met Gly Arg Gly Leu Tyr Arg Ala Phe Pro Val Phe Ala Ala Ala Phe
           1540   1545   1550

Asp Glu Ala Cys Ala Glu Leu Asp Ala His Leu Gly Gln Glu Ile Gly
     1555   1560   1565

Val Arg Glu Val Val Ser Gly Ser Asp Ala Gln Leu Leu Asp Arg Thr
   1570   1575   1580

Leu Trp Ala Gln Ser Gly Leu Phe Ala Leu Gln Val Gly Leu Leu Lys
585   1590   1595   1600

Leu Leu Asp Ser Trp Gly Val Arg Pro Ser Val Val Leu Gly His Ser
            1605   1610   1615

Val Gly Glu Leu Ala Ala Ala Phe Ala Ala Gly Val Val Ser Leu Ser
        1620   1625   1630

Gly Ala Ala Arg Leu Val Ala Gly Arg Ala Arg Leu Met Gln Ala Leu
   1635   1640   1645

Pro Ser Gly Gly Gly Met Leu Ala Val Pro Ala Gly Glu Glu Leu Leu
   1650   1655   1660

Trp Ser Leu Leu Ala Asp Gln Gly Asp Arg Val Gly Ile Ala Ala Val
665   1670   1675   1680

Asn Ala Ala Gly Ser Val Val Leu Ser Gly Asp Arg Asp Val Leu Asp
            1685   1690   1695

Asp Leu Ala Gly Arg Leu Asp Gly Gln Gly Ile Arg Ser Arg Trp Leu
       1700   1705   1710

Arg Val Ser His Ala Phe His Ser Tyr Arg Met Asp Pro Met Leu Ala
       1715   1720   1725

172

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Glu Phe Ala Glu Leu Ala Arg Thr Val Asp Tyr Arg Arg Cys Glu Val
    1730            1735            1740

Pro Ile Val Ser Thr Leu Thr Gly Asp Leu Asp Asp Ala Gly Arg Met
745            1750            1755            1760

Ser Gly Pro Asp Tyr Trp Val Arg Gln Val Arg Glu Pro Val Arg Phe
            1765            1770            1775

Ala Asp Gly Val Gln Ala Leu Val Glu His Asp Val Ala Thr Val Val
            1780            1785            1790

Glu Leu Gly Pro Asp Gly Ala Leu Ser Ala Leu Ile Gln Glu Cys Val
        1795            1800            1805

Ala Ala Ser Asp His Ala Gly Arg Leu Ser Ala Val Pro Ala Met Arg
    1810            1815            1820

Arg Asn Gln Asp Glu Ala Gln Lys Val Met Thr Ala Leu Ala His Val
825            1830            1835            1840

His Val Arg Gly Gly Ala Val Asp Trp Arg Ser Phe Phe Ala Gly Thr
            1845            1850            1855

Arg Ala Lys Gln Ile Glu Leu Pro Thr Tyr Ala Phe Gln Arg Gln Arg
        1860            1865            1870

Tyr Trp Leu Asn Ala Leu Arg Glu Ser Ser Ala Gly Asp Met Gly Arg
        1875            1880            1885

Arg Val Glu Ala Lys Phe Trp Gly Ala Val Glu His Glu Asp Val Glu
    1890            1895            1900

Ser Leu Ala Arg Val Leu Gly Ile Val Asp Asp Gly Ala Ala Val Asp
905            1910            1915            1920

Ser Leu Arg Ser Ala Leu Pro Val Leu Ala Gly Trp Gln Arg Thr Arg
            1925            1930            1935

Thr Thr Glu Ser Ile Met Asp Gln Arg Cys Tyr Arg Ile Gly Trp Arg
        1940            1945            1950

Gln Val Ala Gly Leu Pro Pro Met Gly Thr Val Phe Gly Thr Trp Leu
    1955            1960            1965

Val Phe Ala Pro His Gly Trp Ser Ser Glu Pro Glu Val Val Asp Cys
    1970            1975            1980
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173

Val Thr Ala Leu Arg Ala Arg Gly Ala Ser Val Val Leu Val Glu Ala
985   1990   1995   2000

Asp Pro Asp Pro Thr Ser Phe Gly Asp Arg Val Arg Thr Leu Cys Ser
               2005   2010   2015

Gly Leu Pro Asp Leu Val Gly Val Leu Ser Met Leu Cys Leu Glu Glu
        2020   2025   2030

Ser Val Leu Pro Gly Phe Ser Ala Val Ser Arg Gly Phe Ala Leu Thr
        2035   2040   2045

Val Glu Leu Val Arg Val Leu Arg Ala Ala Gly Ala Thr Ala Arg Leu
   2050   2055   2060

Trp Leu Leu Thr Cys Gly Gly Val Ser Val Gly Asp Val Pro Val Arg
065   2070   2075   2080

Pro Ala Gln Ala Leu Ala Trp Gly Leu Gly Arg Val Val Gly Leu Glu
        2085   2090   2095

His Pro Asp Trp Trp Gly Gly Leu Ile Asp Ile Pro Val Leu Phe Asp
        2100   2105   2110

Glu Asp Ala Gln Glu Arg Leu Ser Ile Val Leu Ala Gly Leu Asp Glu
        2115   2120   2125

Asp Glu Val Ala Ile Arg Pro Asp Gly Met Phe Ala Arg Arg Leu Val
   2130   2135   2140

Arg His Thr Val Ser Ala Asp Val Lys Lys Ala Trp Arg Pro Arg Gly
145   2150   2155   2160

Ser Val Leu Val Thr Gly Gly Thr Gly Gly Leu Gly Ala His Val Ala
        2165   2170   2175

Arg Trp Leu Ala Asp Ala Gly Ala Glu His Val Ala Met Val Ser Arg
        2180   2185   2190

Arg Gly Glu Gln Ala Pro Ser Ala Glu Lys Leu Arg Thr Glu Leu Glu
        2195   2200   2205

Asp Leu Gly Thr Arg Val Ser Ile Val Ser Cys Asp Val Thr Asp Arg
   2210   2215   2220

Glu Ala Leu Ala Glu Val Leu Lys Ala Leu Pro Ala Glu Asn Pro Leu
225   2230   2235   2240

174

```
Thr Ala Val Val His Ala Ala Gly Val Ile Glu Thr Gly Asp Ala Ala
          2245                    2250                 2255

Ala Met Ser Leu Ala Asp Phe Asp His Val Leu Ser Ala Lys Val Ala
          2260                    2265                 2270

Gly Ala Ala Asn Leu Asp Ala Leu Leu Ala Asp Val Glu Leu Asp Ala
          2275                    2280                 2285

Phe Val Leu Phe Ser Ser Val Ser Gly Val Trp Gly Ala Gly Gly His
          2290                    2295                 2300

Gly Ala Tyr Ala Ala Ala Asn Ala Tyr Leu Asp Ala Leu Ala Glu Gln
305                 2310                   2315                 2320

Arg Arg Ser Arg Gly Leu Val Ala Thr Ala Val Ala Trp Gly Pro Trp
              2325                    2330                 2335

Ala Gly Glu Gly Met Ala Ser Gly Glu Thr Gly Asp Gln Leu Arg Arg
              2340                    2345                 2350

Tyr Gly Leu Ser Pro Met Ala Pro Gln His Ala Ile Ala Gly Ile Arg
          2355                    2360                 2365

Gln Ala Val Glu Gln Asp Glu Ile Ser Leu Val Val Ala Asp Val Asp
          2370                    2375                 2380

Trp Ala Arg Phe Ser Ala Gly Leu Leu Ala Ala Arg Pro Arg Pro Leu
385                 2390                   2395                 2400

Leu Asn Glu Leu Ala Glu Val Lys Glu Leu Leu Val Asp Ala Gln Pro
              2405                    2410                 2415

Glu Ala Gly Val Leu Ala Asp Ala Ser Leu Glu Trp Arg Gln Arg Leu
          2420                    2425                 2430

Ser Ala Ala Pro Arg Pro Thr Gln Glu Gln Leu Ile Leu Glu Leu Val
          2435                    2440                 2445

Arg Gly Glu Thr Ala Leu Val Leu Gly His Pro Gly Ala Ala Ala Val
2450                    2455                   2460

Ala Ser Glu Arg Ala Phe Lys Asp Ser Gly Phe Asp Ser Gln Ala Ala
465                 2470                   2475                 2480

Val Glu Leu Arg Val Arg Leu Asn Arg Ala Thr Gly Leu Gln Leu Pro
              2485                    2490                 2495
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 Ser Thr Ile Ile Phe Ser His Pro Thr Pro Ala Glu Leu Ala Ala Glu
          2500              2505              2510


 Leu Arg Ala Arg Leu Leu Pro Glu Ser Ala Gly Ala Gly Ile Pro Glu
          2515              2520              2525


 Glu Asp Glu Ala Arg Ile Arg Ala Ala Leu Thr Ser Ile Pro Phe Pro
          2530              2535              2540


 Ala Leu Arg Glu Ala Gly Leu Val Ser Pro Leu Leu Ala Leu Ala Gly
      545              2550              2555              2560


 His Pro Val Asp Ser Gly Ile Ser Ser Asp Asp Ala Ala Ala Thr Ser
              2565              2570              2575


 Ile Asp Ala Met Asp Val Ala Gly Leu Val Glu Ala Ala Leu Gly Glu
          2580              2585              2590


 Arg Glu Ser
          2595
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<222> (1)..(6456)
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Met Thr Val Thr Thr Ser Tyr Glu Glu Val Val Glu Ala Leu Arg Ala
  1           5                  10                  15


tcg ctc aag gag aac gaa cgc ctc cgg cgc ggc agg gat cgg ttc tcc      96
Ser Leu Lys Glu Asn Glu Arg Leu Arg Arg Gly Arg Asp Arg Phe Ser
              20                  25                  30


gcg gag aag gac gat ccc atc gcg atc gtg gcg atg agt tgt cgt tat     144
Ala Glu Lys Asp Asp Pro Ile Ala Ile Val Ala Met Ser Cys Arg Tyr
          35                  40                  45


ccc ggt cag gtc tcc tcg ccg gag gac ctg tgg caa ctg gct gcc ggc     192
Pro Gly Gln Val Ser Ser Pro Glu Asp Leu Trp Gln Leu Ala Ala Gly
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          50                  55                  60

ggt gtg gac gcg atc tcc gaa gtt ccg ggg gat cgc gga tgg gac ctg    240
Gly Val Asp Ala Ile Ser Glu Val Pro Gly Asp Arg Gly Trp Asp Leu
 65                  70                  75                  80

gat ggc gtg ttc gtt ccg gac tcc gat cgt cct ggc acg tcg tat gcc    288
Asp Gly Val Phe Val Pro Asp Ser Asp Arg Pro Gly Thr Ser Tyr Ala
                     85                  90                  95

tgc gcg ggc ggt ttt ctt cag ggc gtg tcg gag ttc gac gcg ggt ttc    336
Cys Ala Gly Gly Phe Leu Gln Gly Val Ser Glu Phe Asp Ala Gly Phe
                100                 105                 110

ttc ggg att tcg ccg cgt gag gcg ctg gcg atg gat ccg cag cag cgg    384
Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg
            115                 120                 125

ttg ctg ctg gaa gtc gcg tgg gag gtc ttc gag cgg gct ggg ctg gag    432
Leu Leu Leu Glu Val Ala Trp Glu Val Phe Glu Arg Ala Gly Leu Glu
            130                 135                 140

cag cgg tcg aca cgc ggt tcc cgc gtt ggc gtg ttc gtc ggc acc aat    480
Gln Arg Ser Thr Arg Gly Ser Arg Val Gly Val Phe Val Gly Thr Asn
145                 150                 155                 160

ggc cag gac tac gcg tcg tgg ttg cgg acg ccg ccg cct gcg gtg gca    528
Gly Gln Asp Tyr Ala Ser Trp Leu Arg Thr Pro Pro Pro Ala Val Ala
                165                 170                 175

ggt cat gtg ctg acg ggc ggt gcg gca gcg gtt ctt tcg ggc cgg gtt    576
Gly His Val Leu Thr Gly Gly Ala Ala Ala Val Leu Ser Gly Arg Val
            180                 185                 190

gcg tat tcg ttc ggg ttc gag ggt cct gcg gtg acg gtg gat acg gcg    624
Ala Tyr Ser Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr Ala
            195                 200                 205

tgt tcg tcg tcg ttg gtg gcg ttg cac ctg gcg ggg caa gca ctg cgg    672
Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala Gly Gln Ala Leu Arg
            210                 215                 220

gcc ggt gag tgc gac ctt gcc ctt gcc ggt ggc gtc acg gtg atg tcg    720
Ala Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ser
225                 230                 235                 240

acg ccg aag gtg ttc ctg gag ttc tcc cgc caa cgg ggt ctc gcg ccg    768
Thr Pro Lys Val Phe Leu Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro
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                    245                    250                    255

gat ggg cgg tgc aag tcg ttc gcg gcg ggt gcg gat ggc act gga tgg    816
Asp Gly Arg Cys Lys Ser Phe Ala Ala Gly Ala Asp Gly Thr Gly Trp
            260                    265                    270


ggt gag ggt gcc gga ctg ttg ttg ctg gag cgg ttg tcg gat gcc cgg    864
Gly Glu Gly Ala Gly Leu Leu Leu Leu Glu Arg Leu Ser Asp Ala Arg
            275                    280                    285


cgg aat ggg cat gag gtg ctg gcg gtt gtt cgt ggt agt gcg gtg aat    912
Arg Asn Gly His Glu Val Leu Ala Val Val Arg Gly Ser Ala Val Asn
            290                    295                    300


cag gac ggt gcg tcg aat ggt ttg acc gcg ccg aat ggt tcg tcg cag    960
Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Ser Ser Gln
305                    310                    315                    320


cag cgg gtg att acc cag gcg ttg gcg agt gcg ggg ttg tcg gtg tcc   1008
Gln Arg Val Ile Thr Gln Ala Leu Ala Ser Ala Gly Leu Ser Val Ser
                    325                    330                    335


gat gtg gat gct gtg gag gcg cat ggg acg ggc acg cgg ctt ggt gat   1056
Asp Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp
            340                    345                    350


ccg atc gag gcg cag gcg ctg atc gcc acc tac ggc cgt gat cgt gat   1104
Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr Tyr Gly Arg Asp Arg Asp
            355                    360                    365


cct ggc cgg ccg ttg tgg ttg ggg tcg gtc aag tcg aac atc ggt cat   1152
Pro Gly Arg Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile Gly His
            370                    375                    380


acg caa gcg gcg gcg ggt gtg gct ggt gtg atc aag atg gtg atg gcg   1200
Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Met Ala
385                    390                    395                    400


atg cgg cac ggg cag ctg cca cgc acg ttg cac gtg gaa tcg ccg tcg   1248
Met Arg His Gly Gln Leu Pro Arg Thr Leu His Val Glu Ser Pro Ser
                    405                    410                    415


ccg gag gtg gat tgg tcg gcg ggg acg gtt caa ctc ctt acg gag aac   1296
Pro Glu Val Asp Trp Ser Ala Gly Thr Val Gln Leu Leu Thr Glu Asn
            420                    425                    430


acg ccc tgg ccc agg agt ggt cgt gtt cgt cgg gtg ggg gtg tcg tcg   1344
Thr Pro Trp Pro Arg Ser Gly Arg Val Arg Arg Val Gly Val Ser Ser
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             435                     440                     445

ttc ggg atc agt ggt act aac gcg cac gtc atc ctc gaa cag ccc ccg    1392
Phe Gly Ile Ser Gly Thr Asn Ala His Val Ile Leu Glu Gln Pro Pro
    450                     455                     460

gga gtg ccg agt cag tct gcg ggg ccg ggt tcg ggt tct gtc gtg gat    1440
Gly Val Pro Ser Gln Ser Ala Gly Pro Gly Ser Gly Ser Val Val Asp
465                     470                     475                 480

gtt ccg gtg gtg ccg tgg atg gtg tcg ggc aaa aca ccc gaa gcg cta    1488
Val Pro Val Val Pro Trp Met Val Ser Gly Lys Thr Pro Glu Ala Leu
                485                     490                     495

tcc gcg cag gca acg gcg ttg atg acc tat ctg gac gag cga cct gat    1536
Ser Ala Gln Ala Thr Ala Leu Met Thr Tyr Leu Asp Glu Arg Pro Asp
                500                     505                     510

gtc tcc tcg ctg gat gtt ggg tac tcg ctg gcg ttg aca cgg tcg gcg    1584
Val Ser Ser Leu Asp Val Gly Tyr Ser Leu Ala Leu Thr Arg Ser Ala
                515                     520                     525

ctg gat gag cga gcg gtg gtg ctg ggg tcg gac cgt gaa acg ttg ttg    1632
Leu Asp Glu Arg Ala Val Val Leu Gly Ser Asp Arg Glu Thr Leu Leu
    530                     535                     540

tgc ggt gtg aaa gcg ctg tct gcc ggt cat gag gct tct ggg ttg gtg    1680
Cys Gly Val Lys Ala Leu Ser Ala Gly His Glu Ala Ser Gly Leu Val
545                     550                     555                 560

acc gga tct gtg ggg gct ggg ggc cgc atc ggg ttt gtg ttt tcc ggt    1728
Thr Gly Ser Val Gly Ala Gly Gly Arg Ile Gly Phe Val Phe Ser Gly
                565                     570                     575

cag ggt ggt cag tgg ctg ggg atg ggc cgg ggg ctt tac cgg gct ttt    1776
Gln Gly Gly Gln Trp Leu Gly Met Gly Arg Gly Leu Tyr Arg Ala Phe
                580                     585                     590

ccg gtg ttc gct gct gcc ttt gac gaa gct tgt gcc gag ctg gat gca    1824
Pro Val Phe Ala Ala Ala Phe Asp Glu Ala Cys Ala Glu Leu Asp Ala
                595                     600                     605

cat ctg ggc cag gaa atc ggg gtt cgg gag gtg gtg tcc ggt tcg gat    1872
His Leu Gly Gln Glu Ile Gly Val Arg Glu Val Val Ser Gly Ser Asp
        610                     615                     620

gcg cag ttg ctg gat cgg acg ttg tgg gcg cag tcg ggt ttg ttc gcg    1920
Ala Gln Leu Leu Asp Arg Thr Leu Trp Ala Gln Ser Gly Leu Phe Ala
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625   630   635   640

ttg cag gtg ggc ttg ctg aag ttg ctg gat tcg tgg ggg gtt cgg ccg   1968
Leu Gln Val Gly Leu Leu Lys Leu Leu Asp Ser Trp Gly Val Arg Pro
                    645   650   655

agt gtg gtg ttg ggg cat tcg gtg ggc gag ttg gcg gcg gcg ttc gcg   2016
Ser Val Val Leu Gly His Ser Val Gly Glu Leu Ala Ala Ala Phe Ala
                    660   665   670

gcg ggt gtg gtg tcg ttg tcg ggt gcg gct cgg ttg gtg gcg ggt cgt   2064
Ala Gly Val Val Ser Leu Ser Gly Ala Ala Arg Leu Val Ala Gly Arg
                    675   680   685

gcc cgg ttg atg cag gcg ttg ccg tct ggc ggt ggg atg ctg gcg gtg   2112
Ala Arg Leu Met Gln Ala Leu Pro Ser Gly Gly Gly Met Leu Ala Val
                    690   695   700

cct gct ggt gag gag ctg ttg tgg tcg ttg ttg gcc gat cag ggt gat   2160
Pro Ala Gly Glu Glu Leu Leu Trp Ser Leu Leu Ala Asp Gln Gly Asp
705   710   715   720

cgt gtg ggg atc gcc gcg gtc aac gct gcg ggg tcg gtg gtg ctc tct   2208
Arg Val Gly Ile Ala Ala Val Asn Ala Ala Gly Ser Val Val Leu Ser
                    725   730   735

ggt gat cgg gat gtg ctc gat gac ctt gcc ggt cgg ctg gac ggg caa   2256
Gly Asp Arg Asp Val Leu Asp Asp Leu Ala Gly Arg Leu Asp Gly Gln
                    740   745   750

ggg atc cgg tcg agg tgg ttg cgg gtg tcg cat gcg ttt cat tcg tat   2304
Gly Ile Arg Ser Arg Trp Leu Arg Val Ser His Ala Phe His Ser Tyr
                    755   760   765

cgg atg gat ccg atg ctg gcg gag ttc gcc gaa ttg gca cga acc gtg   2352
Arg Met Asp Pro Met Leu Ala Glu Phe Ala Glu Leu Ala Arg Thr Val
                    770   775   780

gat tac cgg cgt tgt gaa gtg ccg atc gtg tcg acc ttg acc gga gac   2400
Asp Tyr Arg Arg Cys Glu Val Pro Ile Val Ser Thr Leu Thr Gly Asp
785   790   795   800

ctc gat gac gct ggc agg atg agc ggg ccc gac tac tgg gtg cgt cag   2448
Leu Asp Asp Ala Gly Arg Met Ser Gly Pro Asp Tyr Trp Val Arg Gln
                    805   810   815

gtg cga gag ccg gtc cgc ttc gcc gac ggt gtc cag gcg ctg gtc gag   2496
Val Arg Glu Pro Val Arg Phe Ala Asp Gly Val Gln Ala Leu Val Glu

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                    820                    825                    830

cac gat gtg gcc act gtt gtc gag ctc ggt ccg gac ggg gcg ttg tcg    2544
His Asp Val Ala Thr Val Val Glu Leu Gly Pro Asp Gly Ala Leu Ser
        835                    840                    845


gcg ctg atc cag gaa tgt gtc gcc gca tcc gat cac gcc ggg cgg ctg    2592
Ala Leu Ile Gln Glu Cys Val Ala Ala Ser Asp His Ala Gly Arg Leu
        850                    855                    860


agc gcg gtc ccg gcg atg cgc agg aac cag gac gag gcg cag aag gtg    2640
Ser Ala Val Pro Ala Met Arg Arg Asn Gln Asp Glu Ala Gln Lys Val
865                    870                    875                    880


atg acg gcc ctg gca cac gtc cac gta cgt ggt ggt gcg gtg gac tgg    2688
Met Thr Ala Leu Ala His Val His Val Arg Gly Gly Ala Val Asp Trp
                    885                    890                    895


cgg tcg ttc ttc gcc ggt acg gga gcg aaa caa atc gag ctg ccc acc    2736
Arg Ser Phe Phe Ala Gly Thr Gly Ala Lys Gln Ile Glu Leu Pro Thr
                900                    905                    910


tac gcc ttc caa cga cag cgg tac tgg ctg gtg cca tcg gat tcc ggt    2784
Tyr Ala Phe Gln Arg Gln Arg Tyr Trp Leu Val Pro Ser Asp Ser Gly
            915                    920                    925


gat gtg aca ggt gcc ggt ctg gcc ggg gcg gag cat ccg ctg ttg ggt    2832
Asp Val Thr Gly Ala Gly Leu Ala Gly Ala Glu His Pro Leu Leu Gly
        930                    935                    940


gct gtg gtg ccg gtc gcg ggt ggt gac gag gtg ttg ctg acc ggc agg    2880
Ala Val Val Pro Val Ala Gly Gly Asp Glu Val Leu Leu Thr Gly Arg
945                    950                    955                    960


att tcg gtg cgg acg cat ccg tgg ctg gcc gaa cac cgg gtg ctg ggt    2928
Ile Ser Val Arg Thr His Pro Trp Leu Ala Glu His Arg Val Leu Gly
                965                    970                    975


gaa gtg atc gtt gcg ggc acc gcg ttg ctg gag atc gcc ttg cac gcg    2976
Glu Val Ile Val Ala Gly Thr Ala Leu Leu Glu Ile Ala Leu His Ala
                980                    985                    990


ggg gaa cgt ctt ggt tgt gaa cgg gtg gaa gag ctc acc ctg gaa gca    3024
Gly Glu Arg Leu Gly Cys Glu Arg Val Glu Glu Leu Thr Leu Glu Ala
            995                    1000                   1005


ccg ctg gtc ctg ccg gag cgc ggg gcg atc cag gtt cag ctg cga gtg    3072
Pro Leu Val Leu Pro Glu Arg Gly Ala Ile Gln Val Gln Leu Arg Val
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181

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              1010                 1015                 1020

     ggc gcg ccc gag aat tcc gga cgc agg ccg atg gcg ctg tat tca cgc      3120
     Gly Ala Pro Glu Asn Ser Gly Arg Arg Pro Met Ala Leu Tyr Ser Arg
     1025                1030            1035                1040


     ccc gaa ggg gcg gcg gag cat gac tgg acg cgg cac gcc acg ggc cgg      3168
     Pro Glu Gly Ala Ala Glu His Asp Trp Thr Arg His Ala Thr Gly Arg
                    1045                1050            1055


     ttg gcg cca ggc cgc ggc gag gcg gct gga gac ctg gcc gac tgg ccg      3216
     Leu Ala Pro Gly Arg Gly Glu Ala Ala Gly Asp Leu Ala Asp Trp Pro
                1060            1065            1070


     gct cct ggc gcg ctg ccg gtc gac ctc gac gaa ttc tat cgg gac ctc      3264
     Ala Pro Gly Ala Leu Pro Val Asp Leu Asp Glu Phe Tyr Arg Asp Leu
            1075            1080            1085


     gca gag ctt ggg ctg gag tac ggc ccg atc ttc caa ggg ctc aag gcg      3312
     Ala Glu Leu Gly Leu Glu Tyr Gly Pro Ile Phe Gln Gly Leu Lys Ala
          1090            1095            1100


     gcc tgg cgg caa ggg gac gag gtg tac gcc gaa gcc gcg ctg ccg gga      3360
     Ala Trp Arg Gln Gly Asp Glu Val Tyr Ala Glu Ala Ala Leu Pro Gly
     1105            1110            1115                1120


     acg gaa gat tct ggt ttc ggg gtg cat ccg gca ctg ctg gac gcg gct      3408
     Thr Glu Asp Ser Gly Phe Gly Val His Pro Ala Leu Leu Asp Ala Ala
                1125            1130            1135


     ctg cac gca acg gct gtc cga gac atg gat gac gca cgc ttg ccg ttc      3456
     Leu His Ala Thr Ala Val Arg Asp Met Asp Asp Ala Arg Leu Pro Phe
                1140            1145            1150


     cag tgg gaa ggt gtg tcc ctg cac gcc aag gcc gcg ccg gct ttg cgg      3504
     Gln Trp Glu Gly Val Ser Leu His Ala Lys Ala Ala Pro Ala Leu Arg
                1155            1160            1165


     gtc cgc gtg gtc ccg gct ggt gac gat gcc aag tcc ctg ctg gtt tgt      3552
     Val Arg Val Val Pro Ala Gly Asp Asp Ala Lys Ser Leu Leu Val Cys
          1170            1175            1180


     gat ggc acc ggt cga ccg gtg atc tcg gtg gac cga ctc gta ttg cgg      3600
     Asp Gly Thr Gly Arg Pro Val Ile Ser Val Asp Arg Leu Val Leu Arg
     1185            1190            1195            1200


     tcg gct gcg gcc cgg cgg acc ggt gcg cgc cga cag gcc cat caa gct      3648
     Ser Ala Ala Ala Arg Arg Thr Gly Ala Arg Arg Gln Ala His Gln Ala
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                    1205                 1210                 1215

cgg ttg tac cgg ttg agc tgg cca acg gtt caa ctg ccg aca tcc gct     3696
Arg Leu Tyr Arg Leu Ser Trp Pro Thr Val Gln Leu Pro Thr Ser Ala
         1220                 1225                 1230

cag cca ccg tcc tgc gtg ctt ctc ggc acc tca gaa gtg tcc gct gac     3744
Gln Pro Pro Ser Cys Val Leu Leu Gly Thr Ser Glu Val Ser Ala Asp
         1235                 1240                 1245

ata cag gtg tat ccg gac ctc cgg tcg ttg acg gct gcg ttg gat gcc     3792
Ile Gln Val Tyr Pro Asp Leu Arg Ser Leu Thr Ala Ala Leu Asp Ala
         1250                 1255                 1260

ggt gcc gaa cca ccc ggc gtc gtc atc gca ccc acg ccc ccc ggc ggt     3840
Gly Ala Glu Pro Pro Gly Val Val Ile Ala Pro Thr Pro Pro Gly Gly
1265                 1270                 1275                 1280

gga cga aca gcg gat gtc cgg gag acg act cgg cat gca ctc gac ctg     3888
Gly Arg Thr Ala Asp Val Arg Glu Thr Thr Arg His Ala Leu Asp Leu
              1285                 1290                 1295

gta caa ggc tgg ctt tcc gat cag cga ctc aac gaa tcc cga ttg ctc     3936
Val Gln Gly Trp Leu Ser Asp Gln Arg Leu Asn Glu Ser Arg Leu Leu
              1300                 1305                 1310

ctg gtg aca cag gga gca gtg gcc gtg gag ccg ggc gaa ccc gtg acc     3984
Leu Val Thr Gln Gly Ala Val Ala Val Glu Pro Gly Glu Pro Val Thr
         1315                 1320                 1325

gat ctg gcg cag gcc gcg ctc tgg gga ctg ctg cgg tcg acg cag acc     4032
Asp Leu Ala Gln Ala Ala Leu Trp Gly Leu Leu Arg Ser Thr Gln Thr
1330                 1335                 1340

gaa cac cct gat cgc ttc gtc ctc gtc gat gtg cct gag ccc gcg caa     4080
Glu His Pro Asp Arg Phe Val Leu Val Asp Val Pro Glu Pro Ala Gln
1345                 1350                 1355                 1360

ctc ctc ccc gcg ctg ccg ggg gtg ctg gcc tgc ggc gaa cct cag ctc     4128
Leu Leu Pro Ala Leu Pro Gly Val Leu Ala Cys Gly Glu Pro Gln Leu
              1365                 1370                 1375

gcg ttg cga cgt ggc ggc gct cat gcg ccc aga ctg gct gga ctg ggc     4176
Ala Leu Arg Arg Gly Gly Ala His Ala Pro Arg Leu Ala Gly Leu Gly
              1380                 1385                 1390

agc gat gac gtc ctg ccc gtg ccg gac ggc acc ggg tgg cga ttg gag     4224
Ser Asp Asp Val Leu Pro Val Pro Asp Gly Thr Gly Trp Arg Leu Glu
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                1395   1400   1405

gcc acg cgc ccg gga agc ctg gat ggg ttg gca ttg gtg gac gaa ccg   4272
Ala Thr Arg Pro Gly Ser Leu Asp Gly Leu Ala Leu Val Asp Glu Pro
    1410   1415   1420

acg gcc acg gca ccg ctg ggt gac ggt gag gtc agg att gcg atg cgc   4320
Thr Ala Thr Ala Pro Leu Gly Asp Gly Glu Val Arg Ile Ala Met Arg
1425   1430   1435   1440

gcg gcc ggg gtg aac ttc cgg gat gcg ctc atc gcg ctc ggt atg tat   4368
Ala Ala Gly Val Asn Phe Arg Asp Ala Leu Ile Ala Leu Gly Met Tyr
            1445   1450   1455

ccc ggt gtg gca tcg ctg ggc agt gag ggc gcc ggg gtc gtg gtg gag   4416
Pro Gly Val Ala Ser Leu Gly Ser Glu Gly Ala Gly Val Val Val Glu
        1460   1465   1470

acc ggc ccc ggc gtc acc ggc ctg gca ccc ggc gac cgc gtg atg gga   4464
Thr Gly Pro Gly Val Thr Gly Leu Ala Pro Gly Asp Arg Val Met Gly
        1475   1480   1485

atg atc ccg aag gcg ttc ggg ccg ctc gcg gtc gcc gac cat cgc atg   4512
Met Ile Pro Lys Ala Phe Gly Pro Leu Ala Val Ala Asp His Arg Met
    1490   1495   1500

gtg acg agg att ccc gct ggt tgg agc ttc gcg cgg gcc gca tcg gtg   4560
Val Thr Arg Ile Pro Ala Gly Trp Ser Phe Ala Arg Ala Ala Ser Val
1505   1510   1515   1520

ccg atc gtc ttt ctc acc gcc tac tac gcg ctg gtt gat ctc gcc ggg   4608
Pro Ile Val Phe Leu Thr Ala Tyr Tyr Ala Leu Val Asp Leu Ala Gly
            1525   1530   1535

ttg aga cca ggg gag tcg ttg ctg gtt cat tcg gcc gcc ggt ggg gtg   4656
Leu Arg Pro Gly Glu Ser Leu Leu Val His Ser Ala Ala Gly Gly Val
            1540   1545   1550

ggg atg gcc gcg atc caa ctc gcc agg cac ctc ggt gca gag gtg tac   4704
Gly Met Ala Ala Ile Gln Leu Ala Arg His Leu Gly Ala Glu Val Tyr
        1555   1560   1565

gcc acc gct agc gag gac aag tgg caa gcc gtg gag ctg agc cga gaa   4752
Ala Thr Ala Ser Glu Asp Lys Trp Gln Ala Val Glu Leu Ser Arg Glu
    1570   1575   1580

cac ctc gct tcg tcg cgg acg tgc gat ttc gag cag cag ttc ctc ggg   4800
His Leu Ala Ser Ser Arg Thr Cys Asp Phe Glu Gln Gln Phe Leu Gly

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      1585              1590              1595              1600

gca acc ggc gga cgc ggc gtc gac gtc gtg ctc aac tcc ctc gcc ggg      4848
Ala Thr Gly Gly Arg Gly Val Asp Val Val Leu Asn Ser Leu Ala Gly
            1605              1610              1615

gag ttc gcc gat gcg tct ctg cga atg ctg ccg cgc ggt ggc cgt ttc      4896
Glu Phe Ala Asp Ala Ser Leu Arg Met Leu Pro Arg Gly Gly Arg Phe
            1620              1625              1630

ctg gag ttg ggg aag acg gat gtt cgt gac ccc gtc gag gtc gcc gat      4944
Leu Glu Leu Gly Lys Thr Asp Val Arg Asp Pro Val Glu Val Ala Asp
         1635              1640              1645

gcg cat ccg ggc gtg tct tac cag gct ttc gat acc gta gag gca ggc      4992
Ala His Pro Gly Val Ser Tyr Gln Ala Phe Asp Thr Val Glu Ala Gly
      1650              1655              1660

ccg cag cga atc ggc gag atg ctt cac gag ctg gtg gag ttg ttc gag      5040
Pro Gln Arg Ile Gly Glu Met Leu His Glu Leu Val Glu Leu Phe Glu
1665              1670              1675              1680

gga cgc gtg ctg gag ccc ctg cct gtc acg gct tgg gac gtt cgg cag      5088
Gly Arg Val Leu Glu Pro Leu Pro Val Thr Ala Trp Asp Val Arg Gln
            1685              1690              1695

gcg ccc gag gcg cta cgg cac ctg agc caa gcg cgg cat gtg gga aag      5136
Ala Pro Glu Ala Leu Arg His Leu Ser Gln Ala Arg His Val Gly Lys
            1700              1705              1710

ctg gtg ctc acc atg cct ccg gtg tgg gac gcc gca ggc acg gtt ctg      5184
Leu Val Leu Thr Met Pro Pro Val Trp Asp Ala Ala Gly Thr Val Leu
         1715              1720              1725

gtt acc ggc gga acg gga gca ctt ggc gca gag gtc gcc cgg cac ctc      5232
Val Thr Gly Gly Thr Gly Ala Leu Gly Ala Glu Val Ala Arg His Leu
      1730              1735              1740

gtg atc gag cgc ggg gtg cga aac ctg gtc ctc gtc agc agg cgc ggt      5280
Val Ile Glu Arg Gly Val Arg Asn Leu Val Leu Val Ser Arg Arg Gly
1745              1750              1755              1760

ccc gca gcc agt ggc gct gct gag ctc gtg gcg caa ctg acg gcc tac      5328
Pro Ala Ala Ser Gly Ala Ala Glu Leu Val Ala Gln Leu Thr Ala Tyr
            1765              1770              1775

ggt gcc gag gtt tcc ttg cag gct tgc gat gtc gcc gat cgt gag acc      5376
Gly Ala Glu Val Ser Leu Gln Ala Cys Asp Val Ala Asp Arg Glu Thr
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              1780                 1785                 1790

ttg gcg aag gtg ctt gcc agc atc ccg gac gag cat ccg ttg acc gcc    5424
Leu Ala Lys Val Leu Ala Ser Ile Pro Asp Glu His Pro Leu Thr Ala
        1795                 1800                 1805

gtg gtg cac gcg gct ggt gtt ctc gac gac gga gtg tcc gaa tcg ctc    5472
Val Val His Ala Ala Gly Val Leu Asp Asp Gly Val Ser Glu Ser Leu
        1810                 1815                 1820

acc gtg gag cgg ctg gac cag gtt ctg cgc ccg aag gtc gat ggc gcg    5520
Thr Val Glu Arg Leu Asp Gln Val Leu Arg Pro Lys Val Asp Gly Ala
1825                 1830                 1835                 1840

cgg aat ctg ctc gag ctg atc gac ccg gac gtg gcc ctc gtg ttg ttc    5568
Arg Asn Leu Leu Glu Leu Ile Asp Pro Asp Val Ala Leu Val Leu Phe
                1845                 1850                 1855

tcg tcg gtg tcg ggt gtg ctc ggc agc ggt ggg cag ggt aac tac gcg    5616
Ser Ser Val Ser Gly Val Leu Gly Ser Gly Gly Gln Gly Asn Tyr Ala
                1860                 1865                 1870

gcg gcc aac tcc ttc ctc gac gca ttg gcg cag caa agg cag tcg cgc    5664
Ala Ala Asn Ser Phe Leu Asp Ala Leu Ala Gln Gln Arg Gln Ser Arg
        1875                 1880                 1885

ggc cta ccg acg aga tca ttg gcc tgg ggg ccc tgg gcg gaa cat ggc    5712
Gly Leu Pro Thr Arg Ser Leu Ala Trp Gly Pro Trp Ala Glu His Gly
        1890                 1895                 1900

atg gcc agc acc ttg cgc gaa gcc gag cag gat cga ttg gcg cga tct    5760
Met Ala Ser Thr Leu Arg Glu Ala Glu Gln Asp Arg Leu Ala Arg Ser
1905                 1910                 1915                 1920

ggg ttg ctg ccg atc tcg acc gag gag ggg ttg tcc cag ttc gac gcc    5808
Gly Leu Leu Pro Ile Ser Thr Glu Glu Gly Leu Ser Gln Phe Asp Ala
                1925                 1930                 1935

gcg tgc ggc ggc gcg cat acc gtg gtg gcg ccg gtt cga ttc agc cgc    5856
Ala Cys Gly Gly Ala His Thr Val Val Ala Pro Val Arg Phe Ser Arg
                1940                 1945                 1950

ttg tcc gac ggg aac gcg atc aag ttc tcc gtc ctg caa ggt ttg gtc    5904
Leu Ser Asp Gly Asn Ala Ile Lys Phe Ser Val Leu Gln Gly Leu Val
        1955                 1960                 1965

ggg ccg cat cgc gtc aac aaa gcg gcg act gcg gat gat gcc gag agc    5952
Gly Pro His Arg Val Asn Lys Ala Ala Thr Ala Asp Asp Ala Glu Ser
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                1970              1975              1980


ctc cgg aaa cgg ttg gga cgc ttg ccg gat gca gaa caa cat cgg att    6000
Leu Arg Lys Arg Leu Gly Arg Leu Pro Asp Ala Glu Gln His Arg Ile
1985              1990              1995              2000


ctg ctg gac ctc gtc cgc atg cat gtg gcg gca gtg ctc gga ttc gcc    6048
Leu Leu Asp Leu Val Arg Met His Val Ala Ala Val Leu Gly Phe Ala
                  2005              2010              2015


ggt tct cag gag atc acc gcg gac ggc acg ttc aag gtg ctg ggc ttc    6096
Gly Ser Gln Glu Ile Thr Ala Asp Gly Thr Phe Lys Val Leu Gly Phe
                  2020              2025              2030


gac tcg ttg acc gtg gtc gag ttg cgc aac cgg atc aac ggg gcg acg    6144
Asp Ser Leu Thr Val Val Glu Leu Arg Asn Arg Ile Asn Gly Ala Thr
     2035              2040              2045


ggg ctg cga ctg ccc gcc acc ctg gtg ttc aac tac ccg acg ccg gat    6192
Gly Leu Arg Leu Pro Ala Thr Leu Val Phe Asn Tyr Pro Thr Pro Asp
     2050              2055              2060


gcg ctc gcc gcg cac ctc gtc acc gcg ctg tcc gca gac cgc ctg gcc    6240
Ala Leu Ala Ala His Leu Val Thr Ala Leu Ser Ala Asp Arg Leu Ala
2065              2070              2075              2080


ggg aca ttc gag gaa ctc gac agg tgg gcg gcg aac ctg ccc acg ctg    6288
Gly Thr Phe Glu Glu Leu Asp Arg Trp Ala Ala Asn Leu Pro Thr Leu
                  2085              2090              2095


gcc agg gat gag gcc acg cgg gcg cag atc acc acc cgg cta cag gcg    6336
Ala Arg Asp Glu Ala Thr Arg Ala Gln Ile Thr Thr Arg Leu Gln Ala
                  2100              2105              2110


atc ttg cag agc ctg gcg gac gtg tcc ggc gga acc ggc ggc ggc tcc    6384
Ile Leu Gln Ser Leu Ala Asp Val Ser Gly Gly Thr Gly Gly Gly Ser
          2115              2120              2125


gtg ccg gac cgg ctc aga tcg gcc acg gac gac gag ctt ttc caa ctc    6432
Val Pro Asp Arg Leu Arg Ser Ala Thr Asp Asp Glu Leu Phe Gln Leu
     2130              2135              2140


ctc gac aac gat ctc gaa ctt ccc tga                                6459
Leu Asp Asn Asp Leu Glu Leu Pro
2145              2150
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<210> 44

<211> 2152
<212> PRT
<213> Saccharopolyspora spinosa

<400> 44
Met Thr Val Thr Thr Ser Tyr Glu Glu Val Val Glu Ala Leu Arg Ala
1   5   10   15

Ser Leu Lys Glu Asn Glu Arg Leu Arg Arg Gly Arg Asp Arg Phe Ser
            20   25   30

Ala Glu Lys Asp Asp Pro Ile Ala Ile Val Ala Met Ser Cys Arg Tyr
            35   40   45

Pro Gly Gln Val Ser Ser Pro Glu Asp Leu Trp Gln Leu Ala Ala Gly
        50   55   60

Gly Val Asp Ala Ile Ser Glu Val Pro Gly Asp Arg Gly Trp Asp Leu
65   70   75   80

Asp Gly Val Phe Val Pro Asp Ser Asp Arg Pro Gly Thr Ser Tyr Ala
                85   90   95

Cys Ala Gly Gly Phe Leu Gln Gly Val Ser Glu Phe Asp Ala Gly Phe
            100   105   110

Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg
            115   120   125

Leu Leu Leu Glu Val Ala Trp Glu Val Phe Glu Arg Ala Gly Leu Glu
        130   135   140

Gln Arg Ser Thr Arg Gly Ser Arg Val Gly Val Phe Val Gly Thr Asn
145   150   155   160

Gly Gln Asp Tyr Ala Ser Trp Leu Arg Thr Pro Pro Pro Ala Val Ala
                165   170   175

Gly His Val Leu Thr Gly Gly Ala Ala Ala Val Leu Ser Gly Arg Val
                180   185   190

Ala Tyr Ser Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr Ala
        195   200   205

Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala Gly Gln Ala Leu Arg
    210   215   220

Ala Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ser

```
       225                 230                 235                 240

    Thr Pro Lys Val Phe Leu Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro
                    245                 250                 255

    Asp Gly Arg Cys Lys Ser Phe Ala Ala Gly Ala Asp Gly Thr Gly Trp
                    260                 265                 270

    Gly Glu Gly Ala Gly Leu Leu Leu Leu Glu Arg Leu Ser Asp Ala Arg
                275                 280                 285

    Arg Asn Gly His Glu Val Leu Ala Val Val Arg Gly Ser Ala Val Asn
                290                 295                 300

    Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Ser Ser Gln
    305                 310                 315                 320

    Gln Arg Val Ile Thr Gln Ala Leu Ala Ser Ala Gly Leu Ser Val Ser
                    325                 330                 335

    Asp Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp
                340                 345                 350

    Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr Tyr Gly Arg Asp Arg Asp
                355                 360                 365

    Pro Gly Arg Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile Gly His
                370                 375                 380

    Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Met Ala
    385                 390                 395                 400

    Met Arg His Gly Gln Leu Pro Arg Thr Leu His Val Glu Ser Pro Ser
                    405                 410                 415

    Pro Glu Val Asp Trp Ser Ala Gly Thr Val Gln Leu Leu Thr Glu Asn
                    420                 425                 430

    Thr Pro Trp Pro Arg Ser Gly Arg Val Arg Arg Val Gly Val Ser Ser
                435                 440                 445

    Phe Gly Ile Ser Gly Thr Asn Ala His Val Ile Leu Glu Gln Pro Pro
                450                 455                 460

    Gly Val Pro Ser Gln Ser Ala Gly Pro Gly Ser Gly Ser Val Val Asp
    465                 470                 475                 480

    Val Pro Val Val Pro Trp Met Val Ser Gly Lys Thr Pro Glu Ala Leu
```

```
                    485                 490                 495

    Ser Ala Gln Ala Thr Ala Leu Met Thr Tyr Leu Asp Glu Arg Pro Asp
                500                 505                 510

    Val Ser Ser Leu Asp Val Gly Tyr·Ser Leu Ala Leu Thr Arg Ser Ala
                515                 520                 525

    Leu Asp Glu Arg Ala Val Val Leu Gly Ser Asp Arg Glu Thr Leu Leu
                530                 535                 540

    Cys Gly Val Lys Ala Leu Ser Ala Gly His Glu Ala Ser Gly Leu Val
    545                 550                 555                 560

    Thr Gly Ser Val Gly Ala Gly Gly Arg Ile Gly Phe Val Phe Ser Gly
                565                 570                 575

    Gln Gly Gly Gln Trp Leu Gly Met Gly Arg Gly Leu Tyr Arg Ala Phe
                580                 585                 590

    Pro Val Phe Ala Ala Ala Phe Asp Glu Ala Cys Ala Glu Leu Asp Ala
                595                 600                 605

    His Leu Gly Gln Glu Ile Gly Val Arg Glu Val Val Ser Gly Ser Asp
        610                 615                 620

    Ala Gln Leu Leu Asp Arg Thr Leu Trp Ala Gln Ser Gly Leu Phe Ala
    625                 630                 635                 640

    Leu Gln Val Gly Leu Leu Lys Leu Leu Asp Ser Trp Gly Val Arg Pro
                645                 650                 655

    Ser Val Val Leu Gly His Ser Val Gly Glu Leu Ala Ala Ala Phe Ala
                660                 665                 670

    Ala Gly Val Val Ser Leu Ser Gly Ala Ala Arg Leu Val Ala Gly Arg
                675                 680                 685

    Ala Arg Leu Met Gln Ala Leu Pro Ser Gly Gly Gly Met Leu Ala Val
        690                 695                 700

    Pro Ala Gly Glu Glu Leu Leu Trp Ser Leu Leu Ala Asp Gln Gly Asp
    705                 710                 715                 720

    Arg Val Gly Ile Ala Ala Val Asn Ala Ala Gly Ser Val Val Leu Ser
                725                 730                 735

    Gly Asp Arg Asp Val Leu Asp Asp Leu Ala Gly Arg Leu Asp Gly Gln
```

                    740   745   750

Gly Ile Arg Ser Arg Trp Leu Arg Val Ser His Ala Phe His Ser Tyr
        755   760   765

Arg Met Asp Pro Met Leu Ala Glu Phe Ala Glu Leu Ala Arg Thr Val
        770   775   780

Asp Tyr Arg Arg Cys Glu Val Pro Ile Val Ser Thr Leu Thr Gly Asp
785   790   795   800

Leu Asp Asp Ala Gly Arg Met Ser Gly Pro Asp Tyr Trp Val Arg Gln
            805   810   815

Val Arg Glu Pro Val Arg Phe Ala Asp Gly Val Gln Ala Leu Val Glu
            820   825   830

His Asp Val Ala Thr Val Val Glu Leu Gly Pro Asp Gly Ala Leu Ser
        835   840   845

Ala Leu Ile Gln Glu Cys Val Ala Ala Ser Asp His Ala Gly Arg Leu
        850   855   860

Ser Ala Val Pro Ala Met Arg Arg Asn Gln Asp Glu Ala Gln Lys Val
865   870   875   880

Met Thr Ala Leu Ala His Val His Val Arg Gly Gly Ala Val Asp Trp
            885   890   895

Arg Ser Phe Phe Ala Gly Thr Gly Ala Lys Gln Ile Glu Leu Pro Thr
            900   905   910

Tyr Ala Phe Gln Arg Gln Arg Tyr Trp Leu Val Pro Ser Asp Ser Gly
        915   920   925

Asp Val Thr Gly Ala Gly Leu Ala Gly Ala Glu His Pro Leu Leu Gly
    930   935   940

Ala Val Val Pro Val Ala Gly Gly Asp Glu Val Leu Leu Thr Gly Arg
945   950   955   960

Ile Ser Val Arg Thr His Pro Trp Leu Ala Glu His Arg Val Leu Gly
        965   970   975

Glu Val Ile Val Ala Gly Thr Ala Leu Leu Glu Ile Ala Leu His Ala
        980   985   990

Gly Glu Arg Leu Gly Cys Glu Arg Val Glu Glu Leu Thr Leu Glu Ala

                            191

```
            995             1000            1005

Pro Leu Val Leu Pro Glu Arg Gly Ala Ile Gln Val Gln Leu Arg Val
    1010             1015             1020

Gly Ala Pro Glu Asn Ser Gly Arg Arg Pro Met Ala Leu Tyr Ser Arg
025              1030             1035             1040

Pro Glu Gly Ala Ala Glu His Asp Trp Thr Arg His Ala Thr Gly Arg
             1045             1050             1055

Leu Ala Pro Gly Arg Gly Glu Ala Ala Gly Asp Leu Ala Asp Trp Pro
         1060             1065             1070

Ala Pro Gly Ala Leu Pro Val Asp Leu Asp Glu Phe Tyr Arg Asp Leu
    1075             1080             1085

Ala Glu Leu Gly Leu Glu Tyr Gly Pro Ile Phe Gln Gly Leu Lys Ala
    1090             1095             1100

Ala Trp Arg Gln Gly Asp Glu Val Tyr Ala Glu Ala Ala Leu Pro Gly
105              1110             1115             1120

Thr Glu Asp Ser Gly Phe Gly Val His Pro Ala Leu Leu Asp Ala Ala
             1125             1130             1135

Leu His Ala Thr Ala Val Arg Asp Met Asp Asp Ala Arg Leu Pro Phe
         1140             1145             1150

Gln Trp Glu Gly Val Ser Leu His Ala Lys Ala Ala Pro Ala Leu Arg
    1155             1160             1165

Val Arg Val Val Pro Ala Gly Asp Asp Ala Lys Ser Leu Leu Val Cys
    1170             1175             1180

Asp Gly Thr Gly Arg Pro Val Ile Ser Val Asp Arg Leu Val Leu Arg
185              1190             1195             1200

Ser Ala Ala Ala Arg Arg Thr Gly Ala Arg Arg Gln Ala His Gln Ala
             1205             1210             1215

Arg Leu Tyr Arg Leu Ser Trp Pro Thr Val Gln Leu Pro Thr Ser Ala
         1220             1225             1230

Gln Pro Pro Ser Cys Val Leu Leu Gly Thr Ser Glu Val Ser Ala Asp
    1235             1240             1245

Ile Gln Val Tyr Pro Asp Leu Arg Ser Leu Thr Ala Ala Leu Asp Ala
```

```
          1250              1255              1260

Gly Ala Glu Pro Pro Gly Val Val Ile Ala Pro Thr Pro Pro Gly Gly
265              1270              1275              1280

Gly Arg Thr Ala Asp Val Arg Glu Thr Thr Arg His Ala Leu Asp Leu
                 1285              1290              1295

Val Gln Gly Trp Leu Ser Asp Gln Arg Leu Asn Glu Ser Arg Leu Leu
                 1300              1305              1310

Leu Val Thr Gln Gly Ala Val Ala Val Glu Pro Gly Glu Pro Val Thr
                 1315              1320              1325

Asp Leu Ala Gln Ala Ala Leu Trp Gly Leu Leu Arg Ser Thr Gln Thr
      1330              1335              1340

Glu His Pro Asp Arg Phe Val Leu Val Asp Val Pro Glu Pro Ala Gln
345              1350              1355              1360

Leu Leu Pro Ala Leu Pro Gly Val Leu Ala Cys Gly Glu Pro Gln Leu
                 1365              1370              1375

Ala Leu Arg Arg Gly Gly Ala His Ala Pro Arg Leu Ala Gly Leu Gly
                 1380              1385              1390

Ser Asp Asp Val Leu Pro Val Pro Asp Gly Thr Gly Trp Arg Leu Glu
                 1395              1400              1405

Ala Thr Arg Pro Gly Ser Leu Asp Gly Leu Ala Leu Val Asp Glu Pro
      1410              1415              1420

Thr Ala Thr Ala Pro Leu Gly Asp Gly Glu Val Arg Ile Ala Met Arg
425              1430              1435              1440

Ala Ala Gly Val Asn Phe Arg Asp Ala Leu Ile Ala Leu Gly Met Tyr
                 1445              1450              1455

Pro Gly Val Ala Ser Leu Gly Ser Glu Gly Ala Gly Val Val Val Glu
                 1460              1465              1470

Thr Gly Pro Gly Val Thr Gly Leu Ala Pro Gly Asp Arg Val Met Gly
      1475              1480              1485

Met Ile Pro Lys Ala Phe Gly Pro Leu Ala Val Ala Asp His Arg Met
      1490              1495              1500

Val Thr Arg Ile Pro Ala Gly Trp Ser Phe Ala Arg Ala Ala Ser Val
```

505   1510   1515   1520

Pro Ile Val Phe Leu Thr Ala Tyr Tyr Ala Leu Val Asp Leu Ala Gly
              1525   1530   1535

Leu Arg Pro Gly Glu Ser Leu Leu Val His Ser Ala Ala Gly Gly Val
              1540   1545   1550

Gly Met Ala Ala Ile Gln Leu Ala Arg His Leu Gly Ala Glu Val Tyr
              1555   1560   1565

Ala Thr Ala Ser Glu Asp Lys Trp Gln Ala Val Glu Leu Ser Arg Glu
            1570   1575   1580

His Leu Ala Ser Ser Arg Thr Cys Asp Phe Glu Gln Gln Phe Leu Gly
585   1590   1595   1600

Ala Thr Gly Gly Arg Gly Val Asp Val Val Leu Asn Ser Leu Ala Gly
              1605   1610   1615

Glu Phe Ala Asp Ala Ser Leu Arg Met Leu Pro Arg Gly Gly Arg Phe
              1620   1625   1630

Leu Glu Leu Gly Lys Thr Asp Val Arg Asp Pro Val Glu Val Ala Asp
              1635   1640   1645

Ala His Pro Gly Val Ser Tyr Gln Ala Phe Asp Thr Val Glu Ala Gly
       1650   1655   1660

Pro Gln Arg Ile Gly Glu Met Leu His Glu Leu Val Glu Leu Phe Glu
665   1670   1675   1680

Gly Arg Val Leu Glu Pro Leu Pro Val Thr Ala Trp Asp Val Arg Gln
              1685   1690   1695

Ala Pro Glu Ala Leu Arg His Leu Ser Gln Ala Arg His Val Gly Lys
            1700   1705   1710

Leu Val Leu Thr Met Pro Pro Val Trp Asp Ala Ala Gly Thr Val Leu
         1715   1720   1725

Val Thr Gly Gly Thr Gly Ala Leu Gly Ala Glu Val Ala Arg His Leu
         1730   1735   1740

Val Ile Glu Arg Gly Val Arg Asn Leu Val Leu Val Ser Arg Arg Gly
745   1750   1755   1760

Pro Ala Ala Ser Gly Ala Ala Glu Leu Val Ala Gln Leu Thr Ala Tyr

194

```
                    1765                1770                1775

    Gly Ala Glu Val Ser Leu Gln Ala Cys Asp Val Ala Asp Arg Glu Thr
            1780                1785         '         1790

    Leu Ala Lys Val Leu Ala Ser Ile Pro Asp Glu His Pro Leu Thr Ala
            1795                1800            1805

    Val Val His Ala Ala Gly Val Leu Asp Asp Gly Val Ser Glu Ser Leu
        1810                1815                1820

    Thr Val Glu Arg Leu Asp Gln Val Leu Arg Pro Lys Val Asp Gly Ala
    825                 1830                1835                1840

    Arg Asn Leu Leu Glu Leu Ile Asp Pro Asp Val Ala Leu Val Leu Phe
            1845                 1850                1855

    Ser Ser Val Ser Gly Val Leu Gly Ser Gly Gly Gln Gly Asn Tyr Ala
            1860                1865                1870

    Ala Ala Asn Ser Phe Leu Asp Ala Leu Ala Gln Gln Arg Gln Ser Arg
            1875                1880                1885

    Gly Leu Pro Thr Arg Ser Leu Ala Trp Gly Pro Trp Ala Glu His Gly
        1890                1895                1900

    Met Ala Ser Thr Leu Arg Glu Ala Glu Gln Asp Arg Leu Ala Arg Ser
    905                 1910                1915                1920

    Gly Leu Leu Pro Ile Ser Thr Glu Glu Gly Leu Ser Gln Phe Asp Ala
            1925                1930                1935

    Ala Cys Gly Gly Ala His Thr Val Val Ala Pro Val Arg Phe Ser Arg
            1940                1945                1950

    Leu Ser Asp Gly Asn Ala Ile Lys Phe Ser Val Leu Gln Gly Leu Val
            1955                1960                1965

    Gly Pro His Arg Val Asn Lys Ala Ala Thr Ala Asp Asp Ala Glu Ser
        1970                1975                1980

    Leu Arg Lys Arg Leu Gly Arg Leu Pro Asp Ala Glu Gln His Arg Ile
    985                 1990                1995                2000

    Leu Leu Asp Leu Val Arg Met His Val Ala Ala Val Leu Gly Phe Ala
            2005                2010                2015

    Gly Ser Gln Glu Ile Thr Ala Asp Gly Thr Phe Lys Val Leu Gly Phe
```

```
                2020              2025              2030

    Asp Ser Leu Thr Val Val Glu Leu Arg Asn Arg Ile Asn Gly Ala Thr
          2035              2040              2045

    Gly Leu Arg Leu Pro Ala Thr Leu Val Phe Asn Tyr Pro Thr Pro Asp
       2050              2055              2060

    Ala Leu Ala Ala His Leu Val Thr Ala Leu Ser Ala Asp Arg Leu Ala
     065              2070              2075              2080

    Gly Thr Phe Glu Glu Leu Asp Arg Trp Ala Ala Asn Leu Pro Thr Leu
             2085              2090              2095

    Ala Arg Asp Glu Ala Thr Arg Ala Gln Ile Thr Thr Arg Leu Gln Ala
             2100              2105              2110

    Ile Leu Gln Ser Leu Ala Asp Val Ser Gly Gly Thr Gly Gly Gly Ser
          2115              2120              2125

    Val Pro Asp Arg Leu Arg Ser Ala Thr Asp Asp Glu Leu Phe Gln Leu
       2130              2135              2140

    Leu Asp Asn Asp Leu Glu Leu Pro
    145              2150
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<210> 45
<211> 9513
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(9510)
<223> ORF20; Polyketidsynthase

<400> 45
atg tcg aat gaa gag aag ctc cgg gag tac ttg cgg cgt gcg ctc gtg      48
Met Ser Asn Glu Glu Lys Leu Arg Glu Tyr Leu Arg Arg Ala Leu Val
 1               5               10              15

gat ctg cac cag gcg cgc gag cgg ctg cac gag gcg gag tcg gga gag     96
Asp Leu His Gln Ala Arg Glu Arg Leu His Glu Ala Glu Ser Gly Glu
              20              25              30

cgg gaa ccc atc gcg atc gtg gcg atg ggc tgc cgg tac ccg ggt ggg    144
```

```
                Arg Glu Pro Ile Ala Ile Val Ala Met Gly Cys Arg Tyr Pro Gly Gly
                         35              40              45

                gtg cag gac ccg gaa ggg ctg tgg aaa ctg gtc gcc tcc ggt ggc gac   192
                Val Gln Asp Pro Glu Gly Leu Trp Lys Leu Val Ala Ser Gly Gly Asp
                         50              55              60

                gcc atc ggt gaa ttc ccc gct gat cgt ggt tgg cac ctc gac gag ctc   240
                Ala Ile Gly Glu Phe Pro Ala Asp Arg Gly Trp His Leu Asp Glu Leu
                65              70              75              80

                tac gat ccc gac ccg gat cag ccc gga acc tgc tac acc cgg cac ggc   288
                Tyr Asp Pro Asp Pro Asp Gln Pro Gly Thr Cys Tyr Thr Arg His Gly
                             85              90              95

                ggc ttc ctc cac gac gcc ggc gag ttc gac gcg gga ttc ttc gac atc   336
                Gly Phe Leu His Asp Ala Gly Glu Phe Asp Ala Gly Phe Phe Asp Ile
                             100             105             110

                agc ccc cgt gag gcg ctc gcg atg gac ccg cag cag cgg ctg ctg ctg   384
                Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu
                             115             120             125

                gaa atc tcc tgg gag acc gtc gaa tcc gct ggg atg gac ccg agg tcc   432
                Glu Ile Ser Trp Glu Thr Val Glu Ser Ala Gly Met Asp Pro Arg Ser
                     130             135             140

                ttg cgg ggg agc cgc acc ggg gtg ttc gcg gga ttg atg tac gag ggc   480
                Leu Arg Gly Ser Arg Thr Gly Val Phe Ala Gly Leu Met Tyr Glu Gly
                145             150             155             160

                tat gac acc ggc gcc cac cgg gca gga gaa ggt gtc gaa ggc tat ctc   528
                Tyr Asp Thr Gly Ala His Arg Ala Gly Glu Gly Val Glu Gly Tyr Leu
                             165             170             175

                gga acc ggc aat gcg gga agc gtc gcc tct ggt cgg gtt gcg tat gcg   576
                Gly Thr Gly Asn Ala Gly Ser Val Ala Ser Gly Arg Val Ala Tyr Ala
                             180             185             190

                ttc ggg ttc gag ggc cca gcg gtg acg gta gac acg gcg tgc tcg tcg   624
                Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser
                             195             200             205

                tcg ttg gtg gcg ctg cat ttg gcg tgt cag tcg ttg cgg cag ggc gag   672
                Ser Leu Val Ala Leu His Leu Ala Cys Gln Ser Leu Arg Gln Gly Glu
                             210             215             220

                tgt gat ctg gcg ctg gcc ggt gga gtg acg gtg atg tcg acg ccg gag   720
```

197

```
Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ser Thr Pro Glu
225             230             235             240


agg ttc gtg gag ttc tcc cgt cag cgt ggt ctc gca ccg gat ggg cgg      768
Arg Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg
            245             250             255


tgt aag tcg ttc gcg gcg gct gcg gat gga acc ggt tgg ggt gag ggt      816
Cys Lys Ser Phe Ala Ala Ala Ala Asp Gly Thr Gly Trp Gly Glu Gly
            260             265             270


gcc ggt ttg gtg ttg ctg gag cgg ctg tca gac gcc agg cgg aac ggg      864
Ala Gly Leu Val Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly
            275             280             285


cat cgg gta ctg gcg gtt gtt cgt ggt agc gcg gtg aat cag gac ggt      912
His Arg Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly
        290             295             300


gcg tcg aac gga ttg acg gcc ccg aac ggg ctg gcc cag gag cgg gtc      960
Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Leu Ala Gln Glu Arg Val
305             310             315             320


att cag cag gtg ctc acg agt gcg ggg ctg tcg gcg tcc gat gtg gac     1008
Ile Gln Gln Val Leu Thr Ser Ala Gly Leu Ser Ala Ser Asp Val Asp
                325             330             335


gct gtg gag gcg cat gga acg ggt acg cgg ctt ggt gat ccg atc gag     1056
Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu
            340             345             350


gcg cag gct ctg ata gcc gcc tat gga cag gat cgg gac cgg gac cgg     1104
Ala Gln Ala Leu Ile Ala Ala Tyr Gly Gln Asp Arg Asp Arg Asp Arg
            355             360             365


ccg ctg tgg ttg ggg tcg gtc aag tcc aac atc ggt cat acg cag gcg     1152
Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile Gly His Thr Gln Ala
        370             375             380


gct gcg ggc gtc gct ggt gtg atc aag atg gtc atg gcg atg cgg cac     1200
Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Met Ala Met Arg His
385             390             395             400


ggg gag ctg ccg cgc acg ttg cac gtg gac gag ccg aat tcg cac gtg     1248
Gly Glu Leu Pro Arg Thr Leu His Val Asp Glu Pro Asn Ser His Val
            405             410             415


gac tgg tcg gct ggt gcg gtc cga ctc ctg acc gag aac atc cgc tgg     1296
Asp Trp Ser Ala Gly Ala Val Arg Leu Leu Thr Glu Asn Ile Arg Trp
```

```
    Asp Trp Ser Ala Gly Ala Val Arg Leu Leu Thr Glu Asn Ile Arg Trp
            420                 425                 430


    cca ggg acg ggt acg cgc cgc gct gga gtg tcg tcg ttc ggg gta agc   1344
    Pro Gly Thr Gly Thr Arg Arg Ala Gly Val Ser Ser Phe Gly Val Ser
            435                 440                 445

    ggt acc aac gca cac gtc atc ctc gaa cac gac ccg ctc gcc gtg acc   1392
    Gly Thr Asn Ala His Val Ile Leu Glu His Asp Pro Leu Ala Val Thr
            450                 455                 460

    gag aac gag gaa gca gcg cag tcc cca gca cct ggg atc gtg ccc tgg   1440
    Glu Asn Glu Glu Ala Ala Gln Ser Pro Ala Pro Gly Ile Val Pro Trp
    465                 470                 475                 480

    gcg ttg tcc ggg cgg tcg tcg acg gcg ctg cgg gcc cag gcc gaa cgg   1488
    Ala Leu Ser Gly Arg Ser Ser Thr Ala Leu Arg Ala Gln Ala Glu Arg
                    485                 490                 495

    ctg cgc gag ctg tgc gag cag acc gat ccc gac ccc gtc gat gtc ggt   1536
    Leu Arg Glu Leu Cys Glu Gln Thr Asp Pro Asp Pro Val Asp Val Gly
                500                 505                 510

    ttc tca ctg gcc gcc acg cgc acg gct tgg gag cac cga gcg gtg gtg   1584
    Phe Ser Leu Ala Ala Thr Arg Thr Ala Trp Glu His Arg Ala Val Val
            515                 520                 525

    ctt ggt cgg gac agc gct acg ttg cgc tcc ggg ctt ggc gtt gtt gcc   1632
    Leu Gly Arg Asp Ser Ala Thr Leu Arg Ser Gly Leu Gly Val Val Ala
            530                 535                 540

    agc ggt gaa cca gcg gtc gat gtc gtt gag ggg agc gtc ctg gac ggc   1680
    Ser Gly Glu Pro Ala Val Asp Val Val Glu Gly Ser Val Leu Asp Gly
    545                 550                 555                 560

    gag gtc gtc ttc gtc ttc ccc ggt cag ggc tgg cag tgg gcc ggt atg   1728
    Glu Val Val Phe Val Phe Pro Gly Gln Gly Trp Gln Trp Ala Gly Met
                    565                 570                 575

    gca gtc gac ctg ctg gac gct tcg ccg acg ttc gcg cgc cac atg gac   1776
    Ala Val Asp Leu Leu Asp Ala Ser Pro Thr Phe Ala Arg His Met Asp
            580                 585                 590

    gag tgc gcc acc gcg ctg cgg agg tac gtg gac tgg tcg ttg gtc gac   1824
    Glu Cys Ala Thr Ala Leu Arg Arg Tyr Val Asp Trp Ser Leu Val Asp
            595                 600                 605

    gtg ctg cgc gga gcg gag aac tcc cca ccg ctg gac cgg gtg gac gtg   1872
```

199

```
Val Leu Arg Gly Ala Glu Asn Ser Pro Pro Leu Asp Arg Val Asp Val
    610                 615             620
```

```
ctc cag ccc gcg tcc ttc gcg gtg atg gtg tcg ctc gcc gag gtg tgg    1920
Leu Gln Pro Ala Ser Phe Ala Val Met Val Ser Leu Ala Glu Val Trp
625                 630             635                 640
```

```
cgt tcc tac ggg gtg agg ccg gcg gcc gtc gtc ggc cac agt caa ggc    1968
Arg Ser Tyr Gly Val Arg Pro Ala Ala Val Val Gly His Ser Gln Gly
                645             650             655
```

```
gaa atc gcc gcg gcc tgc gca gcc ggg gtg ctg ccg ctg gag gat gcg    2016
Glu Ile Ala Ala Ala Cys Ala Ala Gly Val Leu Pro Leu Glu Asp Ala
            660             665             670
```

```
gcc agg ctt gtc gca ttg cgc agc aga gcg ttg aag gga ctt tcg ggg    2064
Ala Arg Leu Val Ala Leu Arg Ser Arg Ala Leu Lys Gly Leu Ser Gly
        675             680             685
```

```
cgg ggt ggc atg gcg tcg ctg gcc tgc cct gcg gat gag gtc gcg gca    2112
Arg Gly Gly Met Ala Ser Leu Ala Cys Pro Ala Asp Glu Val Ala Ala
    690             695             700
```

```
ttg ttc gcg gga tcg ggc ggc cgt ctg gaa gtt gcg gcg atc aac ggc    2160
Leu Phe Ala Gly Ser Gly Gly Arg Leu Glu Val Ala Ala Ile Asn Gly
705             710             715                 720
```

```
ccg cga tcg gtc gtg gtg tcc ggc gat ctg gaa gcg gtg gac gaa ctg    2208
Pro Arg Ser Val Val Val Ser Gly Asp Leu Glu Ala Val Asp Glu Leu
            725             730             735
```

```
ctg gca gag tgc gct gaa aag gac atg cgt gca cgc cgt atc ccc gtc    2256
Leu Ala Glu Cys Ala Glu Lys Asp Met Arg Ala Arg Arg Ile Pro Val
            740             745             750
```

```
gac tac gcc tcg cat tca gcg cac gtg gag gtg gtt cgg agc ccg gtg    2304
Asp Tyr Ala Ser His Ser Ala His Val Glu Val Val Arg Ser Pro Val
        755             760             765
```

```
ctg gcg gcc gcc gcc ggg gtg cga cac cgg gac ggc cag gtg ccg tgg    2352
Leu Ala Ala Ala Ala Gly Val Arg His Arg Asp Gly Gln Val Pro Trp
        770             775             780
```

```
tgg tcg acg gtg atc ggc gac tgg gtg gat ccg gcc agg ctg gac ggc    2400
Trp Ser Thr Val Ile Gly Asp Trp Val Asp Pro Ala Arg Leu Asp Gly
785             790             795                 800
```

```
gag tat tgg tat cgg aac ctc cgg cag ccg gtc cgg ttc gaa cac gcc    2448
```

```
        Glu Tyr Trp Tyr Arg Asn Leu Arg Gln Pro Val Arg Phe Glu His Ala
                        805                 810                 815

        gtg cag ggc ctg gtc gag cgg gga ttc ggc ctg ttc atc gaa atg agt     2496
        Val Gln Gly Leu Val Glu Arg Gly Phe Gly Leu Phe Ile Glu Met Ser
                    820                     825                 830

        gcg cat ccg gtg ctg acc acg gcg gtc gag gaa acc ggt gcg gag tcg     2544
        Ala His Pro Val Leu Thr Thr Ala Val Glu Glu Thr Gly Ala Glu Ser
                    835                     840                 845

        gag acc gcc gtg gcc gcg gta ggt acc ttg cga cgt gac tcg ggc ggc     2592
        Glu Thr Ala Val Ala Ala Val Gly Thr Leu Arg Arg Asp Ser Gly Gly
                850                     855                 860

        ctc cgg agg ttg ttg cat tcg ctg gcc gag gcg tac gtg cgc ggc gcc     2640
        Leu Arg Arg Leu Leu His Ser Leu Ala Glu Ala Tyr Val Arg Gly Ala
        865                     870                 875                 880

        acc gtg gac tgg gcc gtg gcg ttc ggg ggc gcg ggc cga cgg ctg gac     2688
        Thr Val Asp Trp Ala Val Ala Phe Gly Gly Ala Gly Arg Arg Leu Asp
                        885                     890                 895

        ctg ccg acc tac ccg ttc cag cgc cag cgg tac tgg ctg gac aag gga     2736
        Leu Pro Thr Tyr Pro Phe Gln Arg Gln Arg Tyr Trp Leu Asp Lys Gly
                        900                     905                 910

        gct gcc tcc gac gag gct cgt gcg gtc tcg gac ccg gcg gcg ggc tgg     2784
        Ala Ala Ser Asp Glu Ala Arg Ala Val Ser Asp Pro Ala Ala Gly Trp
                    915                     920                 925

        ttc tgg caa gcc gtg gcg cgc caa gac ctg aaa agc gtg tcc gat gcc     2832
        Phe Trp Gln Ala Val Ala Arg Gln Asp Leu Lys Ser Val Ser Asp Ala
                930                     935                 940

        ctc gat ctc gac gcc gac gca ccg ctg agc gca aca ctt cca gcc ctg     2880
        Leu Asp Leu Asp Ala Asp Ala Pro Leu Ser Ala Thr Leu Pro Ala Leu
        945                     950                 955                 960

        tcc gtc tgg cac cgt cag gaa cga gaa agg gtc ttg gca gac ggt tgg     2928
        Ser Val Trp His Arg Gln Glu Arg Glu Arg Val Leu Ala Asp Gly Trp
                        965                 970                     975

        cgg tac cga gtc gac tgg gta cgg gtg gcc ccg cag ccg gtc cgg aga     2976
        Arg Tyr Arg Val Asp Trp Val Arg Val Ala Pro Gln Pro Val Arg Arg
                    980                     985                 990

        acg cgg gaa acc tgg ctc ctg gtc gtt ccc ccg ggc ggc atc gag gaa     3024
```

```
Thr Arg Glu Thr Trp Leu Leu Val Val Pro Pro Gly Gly Ile Glu Glu
        995              1000             1005


gcg ctg gtc gaa cgg ctg acg gat gcg ttg aac acg cga ggg atc agc   3072
Ala Leu Val Glu Arg Leu Thr Asp Ala Leu Asn Thr Arg Gly Ile Ser
    1010              1015             1020


acc ctg cgc ctc gac gtg cca ccg gcg gcg acc agt ggc gaa ctc gca   3120
Thr Leu Arg Leu Asp Val Pro Pro Ala Ala Thr Ser Gly Glu Leu Ala
1025              1030             1035              1040


acc gaa ctc cgc gcc gca gcc gac ggt gac ccg gtg aag gca atc ctg   3168
Thr Glu Leu Arg Ala Ala Ala Asp Gly Asp Pro Val Lys Ala Ile Leu
              1045             1050             1055


tcg ctc acc gcg ttg gac gag cga ccc cac ccc gaa tgc aag gac gtc   3216
Ser Leu Thr Ala Leu Asp Glu Arg Pro His Pro Glu Cys Lys Asp Val
              1060             1065             1070


ccg agc ggg att gcc ttg ctg ctg aac ctg gtc aag gcg ctc ggt gaa   3264
Pro Ser Gly Ile Ala Leu Leu Leu Asn Leu Val Lys Ala Leu Gly Glu
        1075             1080             1085


gcc gac ctc aga att cct ctg tgg acc atc acg cgt ggt gcg gtc aag   3312
Ala Asp Leu Arg Ile Pro Leu Trp Thr Ile Thr Arg Gly Ala Val Lys
    1090             1095             1100


gca ggc ccc gca gat cgg ctg ctg cgc ccg atg cag gcg caa gca tgg   3360
Ala Gly Pro Ala Asp Arg Leu Leu Arg Pro Met Gln Ala Gln Ala Trp
1105             1110             1115              1120


ggt ctg ggg cga gta gcc gca ctc gaa cac ccc gag cgc tgg ggt ggg   3408
Gly Leu Gly Arg Val Ala Ala Leu Glu His Pro Glu Arg Trp Gly Gly
              1125             1130             1135


ctg atc gac ctg ccg gat tcg ctg gac ggc gac gtc ctc acg agg ctg   3456
Leu Ile Asp Leu Pro Asp Ser Leu Asp Gly Asp Val Leu Thr Arg Leu
        1140             1145             1150


ggc gaa gcg ctc acc aac ggc ttg gcg gaa gac caa ctg gcg att cgc   3504
Gly Glu Ala Leu Thr Asn Gly Leu Ala Glu Asp Gln Leu Ala Ile Arg
        1155             1160             1165


cag tcg ggc gtg ctg gcc cgg cga ctg gta ccc gcc ccg gcg aat cag   3552
Gln Ser Gly Val Leu Ala Arg Arg Leu Val Pro Ala Pro Ala Asn Gln
    1170             1175             1180


ccc gct gga cgt aag tgg cgc ccc cga ggg agc gcg ctg atc acg ggc   3600
```

                                   202

```
Pro Ala Gly Arg Lys Trp Arg Pro Arg Gly Ser Ala Leu Ile Thr Gly
1185            1190            1195            1200


gga ctc ggc gcg gtg ggc gca cag gtg gcg agg tgg ttg gcc gaa atc   3648
Gly Leu Gly Ala Val Gly Ala Gln Val Ala Arg Trp Leu Ala Glu Ile
                1205            1210            1215


gga gcc gag cga atc gtg ctc acc agt cga cgg ggc aac caa gca gca   3696
Gly Ala Glu Arg Ile Val Leu Thr Ser Arg Arg Gly Asn Gln Ala Ala
            1220            1225            1230


ggc gcc gcc gag ctg gaa gcc gaa ctc cgg gcc ctt gga gcg caa gtg   3744
Gly Ala Ala Glu Leu Glu Ala Glu Leu Arg Ala Leu Gly Ala Gln Val
        1235            1240            1245


tcc atc gtg gct tgc gac gtg acc gat cgt gcc gag atg tcc gca cta   3792
Ser Ile Val Ala Cys Asp Val Thr Asp Arg Ala Glu Met Ser Ala Leu
    1250            1255            1260


ctg gcc gag ttc gac gtc acc gcg gtg ttc cac gcg gcc gga gtc ggt   3840
Leu Ala Glu Phe Asp Val Thr Ala Val Phe His Ala Ala Gly Val Gly
1265            1270            1275            1280


cgg ctg ctg ccg ttg gcg gag acc gac cag aac ggc ctg gcc gaa ata   3888
Arg Leu Leu Pro Leu Ala Glu Thr Asp Gln Asn Gly Leu Ala Glu Ile
            1285            1290            1295


tgc gcg gcg aag gtc cgc ggc gct cag gtg ctg gac gaa ctg tgc gac   3936
Cys Ala Ala Lys Val Arg Gly Ala Gln Val Leu Asp Glu Leu Cys Asp
            1300            1305            1310


agc acc gat ctc gat gcc ttc gtc ctg ttc tcc tcg ggt gcc ggg gta   3984
Ser Thr Asp Leu Asp Ala Phe Val Leu Phe Ser Ser Gly Ala Gly Val
        1315            1320            1325


tgg ggc ggg ggc ggt cag ggc gct tac ggc gcg gcg aac gca ttc ttg   4032
Trp Gly Gly Gly Gly Gln Gly Ala Tyr Gly Ala Ala Asn Ala Phe Leu
    1330            1335            1340


gac aca ctc gcc gaa caa cgc cga gca cgc ggt ctg ccg gca acc tcg   4080
Asp Thr Leu Ala Glu Gln Arg Arg Ala Arg Gly Leu Pro Ala Thr Ser
1345            1350            1355            1360


atc tcc tgg ggc agt tgg gcc ggc ggc ggc atg gcc gac ggc gcg gcg   4128
Ile Ser Trp Gly Ser Trp Ala Gly Gly Gly Met Ala Asp Gly Ala Ala
            1365            1370            1375


ggc gaa cac ctg cgg cga cgc ggg ata cgt ccg atg ccg gcg gcg tcg   4176
```

203

```
Gly Glu His Leu Arg Arg Arg Gly Ile Arg Pro Met Pro Ala Ala Ser
         1380               1385             1390


gcc atc ctg gct ctg cag gaa gta ctt gac cag gat gag acg tgc gtg     4224
Ala Ile Leu Ala Leu Gln Glu Val Leu Asp Gln Asp Glu Thr Cys Val
         1395               1400             1405


tcg atc gct gat gtg gac tgg gac cga ttc gtt ccc acg ttc gcc gcg     4272
Ser Ile Ala Asp Val Asp Trp Asp Arg Phe Val Pro Thr Phe Ala Ala
         1410               1415             1420


act cgc gcc acc cgg ttg ttc gac gaa gtg ccg gcg gcg aga aag gcg     4320
Thr Arg Ala Thr Arg Leu Phe Asp Glu Val Pro Ala Ala Arg Lys Ala
 1425               1430               1435             1440


atg ccc gcg aat ggg ccg gca gaa cca ggc ggc tcg ccg ttc gcc cgc     4368
Met Pro Ala Asn Gly Pro Ala Glu Pro Gly Gly Ser Pro Phe Ala Arg
             1445               1450             1455


aat ctc gcg gag ctg ccg gaa gcc caa cga cgc cac gaa ctg gtg gat     4416
Asn Leu Ala Glu Leu Pro Glu Ala Gln Arg Arg His Glu Leu Val Asp
             1460               1465             1470


ctg gtg tgc gcc cag gtg gca acc gtg ctc ggg cac ggc agt cgc gag     4464
Leu Val Cys Ala Gln Val Ala Thr Val Leu Gly His Gly Ser Arg Glu
         1475               1480             1485


gaa gtc cag ccc gag cgg gcg ttc cgc gcg ctc ggg ttc gac tcc ctc     4512
Glu Val Gln Pro Glu Arg Ala Phe Arg Ala Leu Gly Phe Asp Ser Leu
         1490               1495             1500


atg gcg gtg gat ctg cgc aat cgt ttg acc acc gcc acc ggg ttg cgc     4560
Met Ala Val Asp Leu Arg Asn Arg Leu Thr Thr Ala Thr Gly Leu Arg
 1505               1510               1515             1520


ctg ccg acc aca acc gtc ttc gac tac ccg aat ccg gcc gcc ttg gcc     4608
Leu Pro Thr Thr Thr Val Phe Asp Tyr Pro Asn Pro Ala Ala Leu Ala
             1525               1530             1535


gct cac ctg ctc gag gag ctg gtg ggt gat gtc gcg tcg gct gcg gtg     4656
Ala His Leu Leu Glu Glu Leu Val Gly Asp Val Ala Ser Ala Ala Val
             1540               1545             1550


acc gct gcc agc gcg ccc gcg agt gac gaa ccg atc gcg atc gtc gcg     4704
Thr Ala Ala Ser Ala Pro Ala Ser Asp Glu Pro Ile Ala Ile Val Ala
         1555               1560             1565


atg agc tgc cgg ttt ccg ggt ggc gcg cac tcg ccg gaa gac ctg tgg     4752
```

```
    Met Ser Cys Arg Phe Pro Gly Gly Ala His Ser Pro Glu Asp Leu Trp
        1570            1575            1580


    cgg ctg gtc gcc gcc ggc acg gag gtg atc ggc gag ttc ccc tcc gac    4800
    Arg Leu Val Ala Ala Gly Thr Glu Val Ile Gly Glu Phe Pro Ser Asp
    1585            1590            1595            1600


    cgg ggc tgg gat gcg gaa ggc ctt tac gat ccg gat gct tcc agg cct    4848
    Arg Gly Trp Asp Ala Glu Gly Leu Tyr Asp Pro Asp Ala Ser Arg Pro
                1605            1610            1615


    gga acg acg tat gcg cgg atg gcg gga ttc ctc tac gac gcc ggt gag    4896
    Gly Thr Thr Tyr Ala Arg Met Ala Gly Phe Leu Tyr Asp Ala Gly Glu
                1620            1625            1630


    ttc gat gcc gac ctg ttc ggc atc agc cca cgt gag gcg ttg gcg atg    4944
    Phe Asp Ala Asp Leu Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met
            1635            1640            1645


    gat ccg cag cag cgg ttg gtg ctc gaa atc gcc tgg gaa gcc ctc gaa    4992
    Asp Pro Gln Gln Arg Leu Val Leu Glu Ile Ala Trp Glu Ala Leu Glu
        1650            1655            1660


    cgg gcc gga atc gat ccg ttg tcc ttg aag ggc agt ggg gtc ggc acg    5040
    Arg Ala Gly Ile Asp Pro Leu Ser Leu Lys Gly Ser Gly Val Gly Thr
    1665            1670            1675            1680


    tac atc ggc gct gga agc cgt ggg tac gcg acg gat gtg cgg cag ttt    5088
    Tyr Ile Gly Ala Gly Ser Arg Gly Tyr Ala Thr Asp Val Arg Gln Phe
                1685            1690            1695


    ccc gag gag gcg gag ggc tac ctg ctg acg ggt acc tcg gcc agt gtg    5136
    Pro Glu Glu Ala Glu Gly Tyr Leu Leu Thr Gly Thr Ser Ala Ser Val
                1700            1705            1710


    ctg tcg ggt cgg gtc gcg tat tcg ttt ggt ttc gag ggt cct gcg gtg    5184
    Leu Ser Gly Arg Val Ala Tyr Ser Phe Gly Phe Glu Gly Pro Ala Val
            1715            1720            1725


    acg gtg gat acg gct tgt tcg tcg tcg ttg gtg gcg ttg cat ctg gcg    5232
    Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala
        1730            1735            1740


    tgc cag tcg ttg cgt tcg ggc gag tgt gat ctg gcg ttg gcc ggt ggt    5280
    Cys Gln Ser Leu Arg Ser Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly
    1745            1750            1755            1760


    gtg acc gtg atg tcg acg ccg gag atg ttc gtg gag ttc tcc cgt cag    5328
```

```
Val Thr Val Met Ser Thr Pro Glu Met Phe Val Glu Phe Ser Arg Gln
         1765                1770                1775 .


cgc ggt ttg gcg ccg gat ggg cgg tgc aag tcg ttc gcg gag agc gcg   5376
Arg Gly Leu Ala Pro Asp Gly Arg Cys Lys Ser Phe Ala Glu Ser Ala
         1780                1785                1790


gac ggc acc ggc tgg ggc gaa ggc gcg ggc ctg ttg ttg ctg gag cgg   5424
Asp Gly Thr Gly Trp Gly Glu Gly Ala Gly Leu Leu Leu Leu Glu Arg
         1795                1800                1805


ttg tcg gac gcc cac cgg aat ggg cat cgg gtg ttg gcg gtg gtt cgt   5472
Leu Ser Asp Ala His Arg Asn Gly His Arg Val Leu Ala Val Val Arg
         1810                1815                1820


ggg tca gcg gtg aat cag gac ggc gcc tcg aac gga ctg gcg gcg ccg   5520
Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Ala Ala Pro
  1825                1830                1835                1840


aac ggt ccg tcg cag cag cgg gtg atc aac cag gca ctc gcg aat gcg   5568
Asn Gly Pro Ser Gln Gln Arg Val Ile Asn Gln Ala Leu Ala Asn Ala
              1845                1850                1855


gct ctt tcg gcg tcc gat gtg gat gcg gtg gag gca cat ggc acc ggg   5616
Ala Leu Ser Ala Ser Asp Val Asp Ala Val Glu Ala His Gly Thr Gly
         1860                1865                1870


acc agg ctg ggt gat ccg atc gag gcg cag gca ttg atc gca acg tat   5664
Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr Tyr
         1875                1880                1885


ggg cag gcc cgg gag cgg gat cgg ccc ttg tgg ctg ggg tcg gtc aag   5712
Gly Gln Ala Arg Glu Arg Asp Arg Pro Leu Trp Leu Gly Ser Val Lys
         1890                1895                1900


tcg aac atc ggt cat acg cag gcc gcg gcg ggt gtt gcc ggt gtg atc   5760
Ser Asn Ile Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile
1905                1910                1915                1920


aag atg gtg atg gcc atg cgg cac ggg cag ctg ccc gcc tcg ctg cac   5808
Lys Met Val Met Ala Met Arg His Gly Gln Leu Pro Ala Ser Leu His
         1925                1930                1935


gcg gat gag ccc acg tcg gag gtc gat tgg tcg tcg ggg gcg gtc cgg   5856
Ala Asp Glu Pro Thr Ser Glu Val Asp Trp Ser Ser Gly Ala Val Arg
         1940                1945                1950


ctc ctc gcc gaa cag gta cct tgg ccg gag tct gac cgt gtt cgt cgg   5904
```

```
Leu Leu Ala Glu Gln Val Pro Trp Pro Glu Ser Asp Arg Val Arg Arg
    1955                1960            1965


gtg ggg gtt tcg tcg ttc ggg atc agc ggc acc aac gca cat gtg atc   5952
Val Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Val Ile
    1970                1975            1980


ctc gaa caa gct acg aat gcg cca gat agt aca gcg gag acg gac aaa   6000
Leu Glu Gln Ala Thr Asn Ala Pro Asp Ser Thr Ala Glu Thr Asp Lys
1985            1990            1995                2000


aca gaa tcc gga tct act gtc gat att ccg gtc gtt ccc tgg ttg gtg   6048
Thr Glu Ser Gly Ser Thr Val Asp Ile Pro Val Val Pro Trp Leu Val
                2005            2010            2015


tcg gga aag acg acg gat tcc ctg cgg gga caa gcc gaa cga gtc ttg   6096
Ser Gly Lys Thr Thr Asp Ser Leu Arg Gly Gln Ala Glu Arg Val Leu
            2020            2025            2030


tct cag gtc gag tcc cgg ccg gag cag cgt tcg ctg gat gtt gcc tac   6144
Ser Gln Val Glu Ser Arg Pro Glu Gln Arg Ser Leu Asp Val Ala Tyr
        2035            2040            2045


tcg ctt gct tct ggc cga gcc gcg ctg gat gaa cgc gct gtc gtg ctg   6192
Ser Leu Ala Ser Gly Arg Ala Ala Leu Asp Glu Arg Ala Val Val Leu
    2050            2055            2060


ggt gcg gac cgc ggt gag ctg gtt gct gga ctg gcg gcg ttg gcc gcc   6240
Gly Ala Asp Arg Gly Glu Leu Val Ala Gly Leu Ala Ala Leu Ala Ala
2065            2070            2075            2080


ggt cag gag gct tct ggg gtg atc agc gga act cgt gct tct gct cgg   6288
Gly Gln Glu Ala Ser Gly Val Ile Ser Gly Thr Arg Ala Ser Ala Arg
            2085            2090            2095


ttc ggg ttc gtg ttc tcg ggg cag ggt ggt cag tgg ttg ggg atg ggc   6336
Phe Gly Phe Val Phe Ser Gly Gln Gly Gly Gln Trp Leu Gly Met Gly
            2100            2105            2110


aga gcg ctc tac tcg aag ttt ccg gtg ttc gct gct gcg ttt gat gag   6384
Arg Ala Leu Tyr Ser Lys Phe Pro Val Phe Ala Ala Ala Phe Asp Glu
        2115            2120            2125


gct tgc gcc gag ttg gag gca cat ctg ggg gaa gac cgc cgg gtt cgg   6432
Ala Cys Ala Glu Leu Glu Ala His Leu Gly Glu Asp Arg Arg Val Arg
    2130            2135            2140


gat gtg gtc ttc ggt tcc gat gcg cag ctg ctg gat cag acg ctg tgg   6480
```

Asp Val Val Phe Gly Ser Asp Ala Gln Leu Leu Asp Gln Thr Leu Trp
2145   2150   2155   2160

gcg cag tcg ggt ctg ttc gcg ctg caa gcc ggc ctc ttg ggg ctg ctg   6528
Ala Gln Ser Gly Leu Phe Ala Leu Gln Ala Gly Leu Leu Gly Leu Leu
               2165   2170   2175

ggt tcg tgg ggc gtt cgg ccg gat gtg gtg atg ggg cat tcg gtc ggg   6576
Gly Ser Trp Gly Val Arg Pro Asp Val Val Met Gly His Ser Val Gly
               2180   2185   2190

gag ttg gcc gcc gcg ttt gcg gct ggc gtg ttg tcg ttg cgg gat gcg   6624
Glu Leu Ala Ala Ala Phe Ala Ala Gly Val Leu Ser Leu Arg Asp Ala
          2195   2200   2205

gct cgg ttg gtg gcc gcg cgc gcc cgg ttg atg caa gcc ctg ccc tct   6672
Ala Arg Leu Val Ala Ala Arg Ala Arg Leu Met Gln Ala Leu Pro Ser
     2210   2215   2220

gac ggc gcg atg ttg gcg gtg gct gct ggt gaa gac ctt gtt cgg cca   6720
Asp Gly Ala Met Leu Ala Val Ala Ala Gly Glu Asp Leu Val Arg Pro
2225   2230   2235   2240

ttg ctg gcc ggt cgg gag gag tcc gtg agc gtc gcc gcg ctc aat gcc   6768
Leu Leu Ala Gly Arg Glu Glu Ser Val Ser Val Ala Ala Leu Asn Ala
               2245   2250   2255

ccc ggt tcg gtg gtg ttg tcg ggc gat cgg gag gtg ctg gcc agc atc   6816
Pro Gly Ser Val Val Leu Ser Gly Asp Arg Glu Val Leu Ala Ser Ile
               2260   2265   2270

gtc ggc cgg ctg acc gag ctc cga gtc cgg acg cgg cgc ttg cgg gtc   6864
Val Gly Arg Leu Thr Glu Leu Arg Val Arg Thr Arg Arg Leu Arg Val
          2275   2280   ·2285

tcc cat gct ttt cat tcg cac cgg atg gac ccg atg ttg ggc gag ttc   6912
Ser His Ala Phe His Ser His Arg Met Asp Pro Met Leu Gly Glu Phe
          2290   2295   2300

gcc cag atc gcc gag tct gcg gag ttc ggt aag cca acg aca ccg ctt   6960
Ala Gln Ile Ala Glu Ser Ala Glu Phe Gly Lys Pro Thr Thr Pro Leu
2305   2310   2315   2320

gtg tcg acg ttg acg ggt gag ctc gac aga gcc gcg gaa atg agc aca   7008
Val Ser Thr Leu Thr Gly Glu Leu Asp Arg Ala Ala Glu Met Ser Thr
               2325   2330   2335

cca ggg tat tgg gtg cgc cag gcg cgt gaa ccc gtc cgt ttc gcc gac   7056

208

```
Pro Gly Tyr Trp Val Arg Gln Ala Arg Glu Pro Val Arg Phe Ala Asp
        2340            2345              2350


ggt gtc cag gcc ctg gca gcg cag ggc ata ggc acg gtc gtc gag ctc    7104
Gly Val Gln Ala Leu Ala Ala Gln Gly Ile Gly Thr Val Val Glu Leu
        2355            2360              2365


ggc ccg gac gga acg ctg gcg gca ctg gtt cgg gag tgt gcg acc gag    7152
Gly Pro Asp Gly Thr Leu Ala Ala Leu Val Arg Glu Cys Ala Thr Glu
        2370            2375              2380


tcc gat cgg gtt ggg cgg att tcg tcg atc cca ctg atg cgc agg gag    7200
Ser Asp Arg Val Gly Arg Ile Ser Ser Ile Pro Leu Met Arg Arg Glu
2385            2390            2395              2400


cgg gac gag acc cgt tcg gtg atg aca gcc ctg gcg cat ctc cac acc    7248
Arg Asp Glu Thr Arg Ser Val Met Thr Ala Leu Ala His Leu His Thr
            2405            2410              2415


cgt ggt ggt gag gtg gac tgg cag gcg ttt ttc gcc ggt acc ggc gct    7296
Arg Gly Gly Glu Val Asp Trp Gln Ala Phe Phe Ala Gly Thr Gly Ala
            2420            2425              2430


agg cag ctc gag ttg cca acg tat gcc ttc caa cga cag cac tac tgg    7344
Arg Gln Leu Glu Leu Pro Thr Tyr Ala Phe Gln Arg Gln His Tyr Trp
        2435            2440              2445


atc gag tcc agt gcg cgg cca gca cgc gac cgc gca gac atc ggc gag    7392
Ile Glu Ser Ser Ala Arg Pro Ala Arg Asp Arg Ala Asp Ile Gly Glu
        2450            2455              2460


gtg gcg gaa cag ttc tgg acc gcg gtt gac caa ggc gat ctg gca acg    7440
Val Ala Glu Gln Phe Trp Thr Ala Val Asp Gln Gly Asp Leu Ala Thr
2465            2470            2475              2480


ttg gtc gcc gct ctg gat ctt ggg gcg gac gac gac aca tgc gca tcg    7488
Leu Val Ala Ala Leu Asp Leu Gly Ala Asp Asp Asp Thr Cys Ala Ser
            2485            2490              2495


ttg agc gat gta ttg ccg gcg ttg tcc tcc tgg cga agc gga ctc cgc    7536
Leu Ser Asp Val Leu Pro Ala Leu Ser Ser Trp Arg Ser Gly Leu Arg
        2500            2505              2510


aac cgt tcg ctc gtc gat tcc tgc cgg tac cga atc agt tgg cat tcc    7584
Asn Arg Ser Leu Val Asp Ser Cys Arg Tyr Arg Ile Ser Trp His Ser
        2515            2520              2525


tct cgg gag gtg ccg gcc ccg aag att tcc ggt acc tgg ctg ttg gtc    7632
```

209

```
      Ser Arg Glu Val Pro Ala Pro Lys Ile Ser Gly Thr Trp Leu Leu Val
         2530            2535            2540


      gtg ccc ggt gct gcg gat gac gga ttg gtc acg gct ttg acg agt tca    7680
      Val Pro Gly Ala Ala Asp Asp Gly Leu Val Thr Ala Leu Thr Ser Ser
      2545            2550            2555            2560


      ctg gtc gga ggc ggc gcc gag gtc gtc cgg atc ggc ctg tcc gaa gag    7728
      Leu Val Gly Gly Gly Ala Glu Val Val Arg Ile Gly Leu Ser Glu Glu
                     2565            2570            2575


      gac ccg cac cgc gag gac gtc gca cag cgg ctg gcc aat gcg ctg acg    7776
      Asp Pro His Arg Glu Asp Val Ala Gln Arg Leu Ala Asn Ala Leu Thr
                2580            2585            2590


      gat gcc ggt caa ctc ggt ggc gtg ctt tcg ctg ttg ggg ctc gat gaa    7824
      Asp Ala Gly Gln Leu Gly Gly Val Leu Ser Leu Leu Gly Leu Asp Glu
            2595            2600            2605


      tcg cct gct ccg gga ttc tcc tgc ttg cca act ggt ttc gcg ctg act    7872
      Ser Pro Ala Pro Gly Phe Ser Cys Leu Pro Thr Gly Phe Ala Leu Thr
         2610            2615            2620


      gtg cag ctt ctg cgg gcc ttg cgg aag gcc gac gtc gag gcg cct ttt    7920
      Val Gln Leu Leu Arg Ala Leu Arg Lys Ala Asp Val Glu Ala Pro Phe
      2625            2630            2635            2640


      tgg gcg gtg acg cgc ggc ggc gtc gcg ttg gaa gat gta cgc gtg tct    7968
      Trp Ala Val Thr Arg Gly Gly Val Ala Leu Glu Asp Val Arg Val Ser
                     2645            2650            2655


      ccg gag cag gcc ctg gtc tgg ggg ctg ctg cgt gtc gcg gga ctg gag    8016
      Pro Glu Gln Ala Leu Val Trp Gly Leu Leu Arg Val Ala Gly Leu Glu
                2660            2665            2670


      cac ccg gag ttc tgg ggt ggc ttg atc gac ctg cca tcg gac tgg gac    8064
      His Pro Glu Phe Trp Gly Gly Leu Ile Asp Leu Pro Ser Asp Trp Asp
            2675            2680            2685


      gac cga ttg ggt gcc cgg ttg gcg ggt gtg ttg gcg gat ggt ggc gag    8112
      Asp Arg Leu Gly Ala Arg Leu Ala Gly Val Leu Ala Asp Gly Gly Glu
         2690            2695            2700


      gat caa gtc gcc att cgc cgt ggt ggt gtg ttc gtg cgg cgg ttg gaa    8160
      Asp Gln Val Ala Ile Arg Arg Gly Gly Val Phe Val Arg Arg Leu Glu
      2705            2710            2715            2720


      cgc gct ggt gcg tcg ggt gcc ggg tcg gtg tgg cgt cct cgg ggg acg    8208
```

.Arg Ala Gly Ala Ser Gly Ala Gly Ser Val Trp Arg Pro Arg Gly Thr
         2725   2730   2735

gtg ttg gtg acg ggt ggt acg ggc ggt ttg ggg gcg cat gtt gcc cgg   8256
Val Leu Val Thr Gly Gly Thr Gly Gly Leu Gly Ala His Val Ala Arg
         2740   2745   2750

tgg ttg gcc ggt gcc ggg gct gag cac gtg gtg ttg acc agc cgt cga   8304
Trp Leu Ala Gly Ala Gly Ala Glu His Val Val Leu Thr Ser Arg Arg
         2755   2760   2765

gga gcg gac gct ccg ggc gct ggg gaa ttg cgg gcg gag ctg gag gcg   8352
Gly Ala Asp Ala Pro Gly Ala Gly Glu Leu Arg Ala Glu Leu Glu Ala
        2770   2775   2780

ctg ggt gct cgg gtg tcg att gtg ccc tgc gac gtg gct gat cgt gac   8400
Leu Gly Ala Arg Val Ser Ile Val Pro Cys Asp Val Ala Asp Arg Asp
2785   2790   2795   2800

gca gtg gct gga gtg ttg gca ggg atc ggt ggg gag tgt ccg ctg act   8448
Ala Val Ala Gly Val Leu Ala Gly Ile Gly Gly Glu Cys Pro Leu Thr
                 2805   2810   2815

gcg gtg gta cac gcc gcc ggg gtc ggc gag gcg ggc gac gta gtg gag   8496
Ala Val Val His Ala Ala Gly Val Gly Glu Ala Gly Asp Val Val Glu
             2820   2825   2830

atg ggt ttg gcg gat ttt gca gcg gtg ttg tcg gtg aag gtg cgt ggt   8544
Met Gly Leu Ala Asp Phe Ala Ala Val Leu Ser Ala Lys Val Arg Gly
         2835   2840   2845

gcg gcg aat ctg gac gag ttg ctg gcc gac tcg gag ctg gat gcg ttt   8592
Ala Ala Asn Leu Asp Glu Leu Leu Ala Asp Ser Glu Leu Asp Ala Phe
     2850   2855   2860

gtg atg ttc tcc tcg gtg tcg ggg gtg tgg gga gcc ggc gga cag ggt   8640
Val Met Phe Ser Ser Val Ser Gly Val Trp Gly Ala Gly Gly Gln Gly
2865   2870   2875   2880

gcg tat gcg gct gcg aac gcc tac ttg gat gcg ttg gcc gag cag cgt   8688
Ala Tyr Ala Ala Ala Asn Ala Tyr Leu Asp Ala Leu Ala Glu Gln Arg
                 2885   2890   2895

cgg gcg agg gga ttg gtc ggg acc gcg gtt gcg tgg gga ccg tgg gcc   8736
Arg Ala Arg Gly Leu Val Gly Thr Ala Val Ala Trp Gly Pro Trp Ala
             2900   2905   2910

ggt gac ggc atg gcc gcc ggc gaa acc ggc gca cag ctg cac cgg atg   8784

211

Gly Asp Gly Met Ala Ala Gly Glu Thr Gly Ala Gln Leu His Arg Met
   2915   2920   2925

ggc ctg gcg tcg atg gaa ccg agc gcg gcg ctg ctg gca ctt cag ggt   8832
Gly Leu Ala Ser Met Glu Pro Ser Ala Ala Leu Leu Ala Leu Gln Gly
   2930   2935   2940

gca ttg gac cgc gat gag acc tcc ctc gtc gtg gcc gat gtc gat tgg   8880
Ala Leu Asp Arg Asp Glu Thr Ser Leu Val Val Ala Asp Val Asp Trp
2945   2950   2955   2960

gca cgg ttc gcc cca gcc ttc acc tcg gca cgt cga cgc ccg ctg ctg   8928
Ala Arg Phe Ala Pro Ala Phe Thr Ser Ala Arg Arg Arg Pro Leu Leu
           2965   2970   2975

gac acc atc gac gag gcc cga gcc gca ttg gaa acc acc ggc gaa caa   8976
Asp Thr Ile Asp Glu Ala Arg Ala Ala Leu Glu Thr Thr Gly Glu Gln
           2980   2985   2990

gcg ggc aca ggc aaa ccc gtt gag ctg acg caa cgc ctg gcc gga ctg   9024
Ala Gly Thr Gly Lys Pro Val Glu Leu Thr Gln Arg Leu Ala Gly Leu
           2995   3000   3005

tcg cgg aag gaa cgc gac gat gcg gta ttg gat ctg gtg cgg gcg gag   9072
Ser Arg Lys Glu Arg Asp Asp Ala Val Leu Asp Leu Val Arg Ala Glu
   3010   3015   3020

acg gcg gct gtg ctg gga cgc gac gat gcc acg gcc ctg gcg cca tcg   9120
Thr Ala Ala Val Leu Gly Arg Asp Asp Ala Thr Ala Leu Ala Pro Ser
3025   3030   3035   3040

cgg ccg ttc cag gaa ctc gga ttc gac tcc ttg atg gcg gtg gag ctg   9168
Arg Pro Phe Gln Glu Leu Gly Phe Asp Ser Leu Met Ala Val Glu Leu
           3045   3050   3055

cgc aac cgg ctg aac acc gcc acc ggg atc cag ctg ccc gcc agc acg   9216
Arg Asn Arg Leu Asn Thr Ala Thr Gly Ile Gln Leu Pro Ala Ser Thr
           3060   3065   3070

att ttc gac tac ccc aat gcc gag tcg ctg tcg cgt cac ctc tgc gcc   9264
Ile Phe Asp Tyr Pro Asn Ala Glu Ser Leu Ser Arg His Leu Cys Ala
           3075   3080   3085

gag ctt ttc cca acg gag act acc gtg gac tcg gcc ctt gcc gag ctc   9312
Glu Leu Phe Pro Thr Glu Thr Thr Val Asp Ser Ala Leu Ala Glu Leu
           3090   3095   3100

gat cga atc gag cag cag ctc tcg atg ctc acc ggc gaa gcg cgg gca   9360

212

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Asp Arg Ile Glu Gln Gln Leu Ser Met Leu Thr Gly Glu Ala Arg Ala
3105            3110            3115            3120

cgg gac cga atc gcg aca cga ctg cga gcc ctc cac gag aag tgg aac    9408
Arg Asp Arg Ile Ala Thr Arg Leu Arg Ala Leu His Glu Lys Trp Asn
            3125            3130            3135

agc gca gct gaa gta ccg acc gga gcc gat gtc ctg agc acg ctc gat    9456
Ser Ala Ala Glu Val Pro Thr Gly Ala Asp Val Leu Ser Thr Leu Asp
            3140            3145            3150

tcg gcg acg cac gac gag ata ttc gag ttc atc gac aac gag ctc gac    9504
Ser Ala Thr His Asp Glu Ile Phe Glu Phe Ile Asp Asn Glu Leu Asp
            3155            3160            3165

ctg tcc tga                                                        9513
Leu Ser
    3170
```

<210> 46
<211> 3170
<212> PRT
<213> Saccharopolyspora spinosa

<400> 46
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Met Ser Asn Glu Glu Lys Leu Arg Glu Tyr Leu Arg Arg Ala Leu Val
 1               5              10              15

Asp Leu His Gln Ala Arg Glu Arg Leu His Glu Ala Glu Ser Gly Glu
            20              25              30

Arg Glu Pro Ile Ala Ile Val Ala Met Gly Cys Arg Tyr Pro Gly Gly
        35              40              45

Val Gln Asp Pro Glu Gly Leu Trp Lys Leu Val Ala Ser Gly Gly Asp
    50              55              60

Ala Ile Gly Glu Phe Pro Ala Asp Arg Gly Trp His Leu Asp Glu Leu
65              70              75              80

Tyr Asp Pro Asp Pro Asp Gln Pro Gly Thr Cys Tyr Thr Arg His Gly
            85              90              95

Gly Phe Leu His Asp Ala Gly Glu Phe Asp Ala Gly Phe Phe Asp Ile
            100             105             110

Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu
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            115              120              125

Glu Ile Ser Trp Glu Thr Val Glu Ser Ala Gly Met Asp Pro Arg Ser
    130              135              140

Leu Arg Gly Ser Arg Thr Gly Val Phe Ala Gly Leu Met Tyr Glu Gly
145              150              155              160

Tyr Asp Thr Gly Ala His Arg Ala Gly Glu Gly Val Glu Gly Tyr Leu
                165              170              175

Gly Thr Gly Asn Ala Gly Ser Val Ala Ser Gly Arg Val Ala Tyr Ala
            180              185              190

Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser
    195              200              205

Ser Leu Val Ala Leu His Leu Ala Cys Gln Ser Leu Arg Gln Gly Glu
    210              215              220

Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ser Thr Pro Glu
225              230              235              240

Arg Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg
            245              250              255

Cys Lys Ser Phe Ala Ala Ala Ala Asp Gly Thr Gly Trp Gly Glu Gly
            260              265              270

Ala Gly Leu Val Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly
    275              280              285

His Arg Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly
    290              295              300

Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Leu Ala Gln Glu Arg Val
305              310              315              320

Ile Gln Gln Val Leu Thr Ser Ala Gly Leu Ser Ala Ser Asp Val Asp
            325              330              335

Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly Asp Pro Ile Glu
            340              345              350

Ala Gln Ala Leu Ile Ala Ala Tyr Gly Gln Asp Arg Asp Arg Asp Arg
    355              360              365

Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile Gly His Thr Gln Ala
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            370                    375                    380

Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Met Ala Met Arg His
385                 390                 395                 400

Gly Glu Leu Pro Arg Thr Leu His Val Asp Glu Pro Asn Ser His Val
                405                 410                 415

Asp Trp Ser Ala Gly Ala Val Arg Leu Leu Thr Glu Asn Ile Arg Trp
                420                 425                 430

Pro Gly Thr Gly Thr Arg Arg Ala Gly Val Ser Ser Phe Gly Val Ser
                435                 440                 445

Gly Thr Asn Ala His Val Ile Leu Glu His Asp Pro Leu Ala Val Thr
            450                 455                 460

Glu Asn Glu Glu Ala Ala Gln Ser Pro Ala Pro Gly Ile Val Pro Trp
465                 470                 475                 480

Ala Leu Ser Gly Arg Ser Ser Thr Ala Leu Arg Ala Gln Ala Glu Arg
                485                 490                 495

Leu Arg Glu Leu Cys Glu Gln Thr Asp Pro Asp Pro Val Asp Val Gly
            500                 505                 510

Phe Ser Leu Ala Ala Thr Arg Thr Ala Trp Glu His Arg Ala Val Val
            515                 520                 525

Leu Gly Arg Asp Ser Ala Thr Leu Arg Ser Gly Leu Gly Val Val Ala
            530                 535                 540

Ser Gly Glu Pro Ala Val Asp Val Val Glu Gly Ser Val Leu Asp Gly
545                 550                 555                 560

Glu Val Val Phe Val Phe Pro Gly Gln Gly Trp Gln Trp Ala Gly Met
                565                 570                 575

Ala Val Asp Leu Leu Asp Ala Ser Pro Thr Phe Ala Arg His Met Asp
                580                 585                 590

Glu Cys Ala Thr Ala Leu Arg Arg Tyr Val Asp Trp Ser Leu Val Asp
            595                 600                 605

Val Leu Arg Gly Ala Glu Asn Ser Pro Pro Leu Asp Arg Val Asp Val
            610                 615                 620

Leu Gln Pro Ala Ser Phe Ala Val Met Val Ser Leu Ala Glu Val Trp
```

                625   630   635   640

Arg Ser Tyr Gly Val Arg Pro Ala Ala Val Val Gly His Ser Gln Gly
                    645   . 650   655

Glu Ile Ala Ala Ala Cys Ala Ala Gly Val Leu Pro Leu Glu Asp Ala
            660   665   670

Ala Arg Leu Val Ala Leu Arg Ser Arg Ala Leu Lys Gly Leu Ser Gly
            675   680   685

Arg Gly Gly Met Ala Ser Leu Ala Cys Pro Ala Asp Glu Val Ala Ala
            690   695   700

Leu Phe Ala Gly Ser Gly Gly Arg Leu Glu Val Ala Ala Ile Asn Gly
705   710   715   720

Pro Arg Ser Val Val Val Ser Gly Asp Leu Glu Ala Val Asp Glu Leu
                    725   730   735

Leu Ala Glu Cys Ala Glu Lys Asp Met Arg Ala Arg Arg Ile Pro Val
            740   745   750

Asp Tyr Ala Ser His Ser Ala His Val Glu Val Val Arg Ser Pro Val
            755   760   765

Leu Ala Ala Ala Ala Gly Val Arg His Arg Asp Gly Gln Val Pro Trp
            770   775   780

Trp Ser Thr Val Ile Gly Asp Trp Val Asp Pro Ala Arg Leu Asp Gly
785   790   795   800

Glu Tyr Trp Tyr Arg Asn Leu Arg Gln Pro Val Arg Phe Glu His Ala
                    805   810   815

Val Gln Gly Leu Val Glu Arg Gly Phe Gly Leu Phe Ile Glu Met Ser
            820   825   830

Ala His Pro Val Leu Thr Thr Ala Val Glu Glu Thr Gly Ala Glu Ser
            835   840   845

Glu Thr Ala Val Ala Ala Val Gly Thr Leu Arg Arg Asp Ser Gly Gly
            850   855   860

Leu Arg Arg Leu Leu His Ser Leu Ala Glu Ala Tyr Val Arg Gly Ala
865   870   875   880

Thr Val Asp Trp Ala Val Ala Phe Gly Gly Ala Gly Arg Arg Leu Asp

                                216

                    885   890   895

Leu Pro Thr Tyr Pro Phe Gln Arg Gln Arg Tyr Trp Leu Asp Lys Gly
              900   905   910

Ala Ala Ser Asp Glu Ala Arg Ala Val Ser Asp Pro Ala Ala Gly Trp
          915   920   925

Phe Trp Gln Ala Val Ala Arg Gln Asp Leu Lys Ser Val Ser Asp Ala
          930   935   940

Leu Asp Leu Asp Ala Asp Ala Pro Leu Ser Ala Thr Leu Pro Ala Leu
945   950   955   960

Ser Val Trp His Arg Gln Glu Arg Glu Arg Val Leu Ala Asp Gly Trp
              965   970   975

Arg Tyr Arg Val Asp Trp Val Arg Val Ala Pro Gln Pro Val Arg Arg
              980   985   990

Thr Arg Glu Thr Trp Leu Leu Val Val Pro Pro Gly Gly Ile Glu Glu
          995   1000   1005

Ala Leu Val Glu Arg Leu Thr Asp Ala Leu Asn Thr Arg Gly Ile Ser
    1010   1015   1020

Thr Leu Arg Leu Asp Val Pro Pro Ala Ala Thr Ser Gly Glu Leu Ala
025   1030   1035   1040

Thr Glu Leu Arg Ala Ala Ala Asp Gly Asp Pro Val Lys Ala Ile Leu
              1045   1050   1055

Ser Leu Thr Ala Leu Asp Glu Arg Pro His Pro Glu Cys Lys Asp Val
          1060   1065   1070

Pro Ser Gly Ile Ala Leu Leu Leu Asn Leu Val Lys Ala Leu Gly Glu
          1075   1080   1085

Ala Asp Leu Arg Ile Pro Leu Trp Thr Ile Thr Arg Gly Ala Val Lys
    1090   1095   1100

Ala Gly Pro Ala Asp Arg Leu Leu Arg Pro Met Gln Ala Gln Ala Trp
105   1110   1115   1120

Gly Leu Gly Arg Val Ala Ala Leu Glu His Pro Glu Arg Trp Gly Gly
              1125   1130   1135

Leu Ile Asp Leu Pro Asp Ser Leu Asp Gly Asp Val Leu Thr Arg Leu

                                217

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              1140                1145                1150

Gly Glu Ala Leu Thr Asn Gly Leu Ala Glu Asp Gln Leu Ala Ile Arg
      1155              1160                1165

Gln Ser Gly Val Leu Ala Arg Arg Leu Val Pro Ala Pro Ala Asn Gln
    1170              1175              1180

Pro Ala Gly Arg Lys Trp Arg Pro Arg Gly Ser Ala Leu Ile Thr Gly
185             1190              1195              1200

Gly Leu Gly Ala Val Gly Ala Gln Val Ala Arg Trp Leu Ala Glu Ile
          1205              1210              1215

Gly Ala Glu Arg Ile Val Leu Thr Ser Arg Arg Gly Asn Gln Ala Ala
        1220              1225              1230

Gly Ala Ala Glu Leu Glu Ala Glu Leu Arg Ala Leu Gly Ala Gln Val
      1235              1240              1245

Ser Ile Val Ala Cys Asp Val Thr Asp Arg Ala Glu Met Ser Ala Leu
    1250              1255              1260

Leu Ala Glu Phe Asp Val Thr Ala Val Phe His Ala Ala Gly Val Gly
265             1270              1275              1280

Arg Leu Leu Pro Leu Ala Glu Thr Asp Gln Asn Gly Leu Ala Glu Ile
          1285              1290              1295

Cys Ala Ala Lys Val Arg Gly Ala Gln Val Leu Asp Glu Leu Cys Asp
        1300              1305              1310

Ser Thr Asp Leu Asp Ala Phe Val Leu Phe Ser Ser Gly Ala Gly Val
      1315              1320              1325

Trp Gly Gly Gly Gly Gln Gly Ala Tyr Gly Ala Ala Asn Ala Phe Leu
    1330              1335              1340

Asp Thr Leu Ala Glu Gln Arg Arg Ala Arg Gly Leu Pro Ala Thr Ser
345             1350              1355              1360

Ile Ser Trp Gly Ser Trp Ala Gly Gly Gly Met Ala Asp Gly Ala Ala
          1365              1370              1375

Gly Glu His Leu Arg Arg Arg Gly Ile Arg Pro Met Pro Ala Ala Ser
        1380              1385              1390

Ala Ile Leu Ala Leu Gln Glu Val Leu Asp Gln Asp Glu Thr Cys Val
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            1395                1400                1405

Ser Ile Ala Asp Val Asp Trp Asp Arg Phe Val Pro Thr Phe Ala Ala
    1410                1415                1420

Thr Arg Ala Thr Arg Leu Phe Asp Glu Val Pro Ala Ala Arg Lys Ala
425                1430                1435                1440

Met Pro Ala Asn Gly Pro Ala Glu Pro Gly Gly Ser Pro Phe Ala Arg
                1445                1450                1455

Asn Leu Ala Glu Leu Pro Glu Ala Gln Arg Arg His Glu Leu Val Asp
            1460                1465                1470

Leu Val Cys Ala Gln Val Ala Thr Val Leu Gly His Gly Ser Arg Glu
            1475                1480                1485

Glu Val Gln Pro Glu Arg Ala Phe Arg Ala Leu Gly Phe Asp Ser Leu
        1490                1495                1500

Met Ala Val Asp Leu Arg Asn Arg Leu Thr Thr Ala Thr Gly Leu Arg
505                1510                1515                1520

Leu Pro Thr Thr Thr Val Phe Asp Tyr Pro Asn Pro Ala Ala Leu Ala
            1525                1530                1535

Ala His Leu Leu Glu Glu Leu Val Gly Asp Val Ala Ser Ala Ala Val
            1540                1545                1550

Thr Ala Ala Ser Ala Pro Ala Ser Asp Glu Pro Ile Ala Ile Val Ala
        1555                1560                1565

Met Ser Cys Arg Phe Pro Gly Gly Ala His Ser Pro Glu Asp Leu Trp
    1570                1575                1580

Arg Leu Val Ala Ala Gly Thr Glu Val Ile Gly Glu Phe Pro Ser Asp
585                1590                1595                1600

Arg Gly Trp Asp Ala Glu Gly Leu Tyr Asp Pro Asp Ala Ser Arg Pro
            1605                1610                1615

Gly Thr Thr Tyr Ala Arg Met Ala Gly Phe Leu Tyr Asp Ala Gly Glu
            1620                1625                1630

Phe Asp Ala Asp Leu Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met
        1635                1640                1645

Asp Pro Gln Gln Arg Leu Val Leu Glu Ile Ala Trp Glu Ala Leu Glu
```

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         1650              1655              1660

Arg Ala Gly Ile Asp Pro Leu Ser Leu Lys Gly Ser Gly Val Gly Thr
665             1670              1675              1680

Tyr Ile Gly Ala Gly Ser Arg Gly Tyr Ala Thr Asp Val Arg Gln Phe
             1685              1690              1695

Pro Glu Glu Ala Glu Gly Tyr Leu Leu Thr Gly Thr Ser Ala Ser Val
             1700              1705              1710

Leu Ser Gly Arg Val Ala Tyr Ser Phe Gly Phe Glu Gly Pro Ala Val
             1715              1720              1725

Thr Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala
             1730              1735              1740

Cys Gln Ser Leu Arg Ser Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly
745             1750              1755              1760

Val Thr Val Met Ser Thr Pro Glu Met Phe Val Glu Phe Ser Arg Gln
             1765              1770              1775

Arg Gly Leu Ala Pro Asp Gly Arg Cys Lys Ser Phe Ala Glu Ser Ala
             1780              1785              1790

Asp Gly Thr Gly Trp Gly Glu Gly Ala Gly Leu Leu Leu Leu Glu Arg
             1795              1800              1805

Leu Ser Asp Ala His Arg Asn Gly His Arg Val Leu Ala Val Val Arg
             1810              1815              1820

Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Ala Ala Pro
825             1830              1835              1840

Asn Gly Pro Ser Gln Gln Arg Val Ile Asn Gln Ala Leu Ala Asn Ala
             1845              1850              1855

Ala Leu Ser Ala Ser Asp Val Asp Ala Val Glu Ala His Gly Thr Gly
             1860              1865              1870

Thr Arg Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr Tyr
             1875              1880              1885

Gly Gln Ala Arg Glu Arg Asp Arg Pro Leu Trp Leu Gly Ser Val Lys
             1890              1895              1900

Ser Asn Ile Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile
```

905   1910   1915   1920

Lys Met Val Met Ala Met Arg His Gly Gln Leu Pro Ala Ser Leu His
         1925   1930   1935

Ala Asp Glu Pro Thr Ser Glu Val Asp Trp Ser Ser Gly Ala Val Arg
         1940   1945   1950

Leu Leu Ala Glu Gln Val Pro Trp Pro Glu Ser Asp Arg Val Arg Arg
         1955   1960   1965

Val Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Val Ile
         1970   1975   1980

Leu Glu Gln Ala Thr Asn Ala Pro Asp Ser Thr Ala Glu Thr Asp Lys
985   1990   1995   2000

Thr Glu Ser Gly Ser Thr Val Asp Ile Pro Val Val Pro Trp Leu Val
             2005   2010   2015

Ser Gly Lys Thr Thr Asp Ser Leu Arg Gly Gln Ala Glu Arg Val Leu
         2020   2025   2030

Ser Gln Val Glu Ser Arg Pro Glu Gln Arg Ser Leu Asp Val Ala Tyr
         2035   2040   2045

Ser Leu Ala Ser Gly Arg Ala Ala Leu Asp Glu Arg Ala Val Val Leu
         2050   2055   2060

Gly Ala Asp Arg Gly Glu Leu Val Ala Gly Leu Ala Ala Leu Ala Ala
065   2070   2075   2080

Gly Gln Glu Ala Ser Gly Val Ile Ser Gly Thr Arg Ala Ser Ala Arg
             2085   2090   2095

Phe Gly Phe Val Phe Ser Gly Gln Gly Gly Gln Trp Leu Gly Met Gly
             2100   2105   2110

Arg Ala Leu Tyr Ser Lys Phe Pro Val Phe Ala Ala Ala Phe Asp Glu
         2115   2120   2125

Ala Cys Ala Glu Leu Glu Ala His Leu Gly Glu Asp Arg Arg Val Arg
         2130   2135   2140

Asp Val Val Phe Gly Ser Asp Ala Gln Leu Leu Asp Gln Thr Leu Trp
145   2150   2155   2160

Ala Gln Ser Gly Leu Phe Ala Leu Gln Ala Gly Leu Leu Gly Leu Leu

221

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              2165                2170                2175
Gly Ser Trp Gly Val Arg Pro Asp Val Val Met Gly His Ser Val Gly
         2180                2185                2190
Glu Leu Ala Ala Ala Phe Ala Ala Gly Val Leu Ser Leu Arg Asp Ala
         2195                2200                2205
Ala Arg Leu Val Ala Ala Arg Ala Arg Leu Met Gln Ala Leu Pro Ser
      2210                2215                2220
Asp Gly Ala Met Leu Ala Val Ala Ala Gly Glu Asp Leu Val Arg Pro
   225                2230                2235                2240
Leu Leu Ala Gly Arg Glu Glu Ser Val Ser Val Ala Ala Leu Asn Ala
             2245                2250                2255
Pro Gly Ser Val Val Leu Ser Gly Asp Arg Glu Val Leu Ala Ser Ile
         2260                2265                2270
Val Gly Arg Leu Thr Glu Leu Arg Val Arg Thr Arg Arg Leu Arg Val
         2275                2280                2285
Ser His Ala Phe His Ser His Arg Met Asp Pro Met Leu Gly Glu Phe
      2290                2295                2300
Ala Gln Ile Ala Glu Ser Ala Glu Phe Gly Lys Pro Thr Thr Pro Leu
   305                2310                2315                2320
Val Ser Thr Leu Thr Gly Glu Leu Asp Arg Ala Ala Glu Met Ser Thr
             2325                2330                2335
Pro Gly Tyr Trp Val Arg Gln Ala Arg Glu Pro Val Arg Phe Ala Asp
             2340                2345                2350
Gly Val Gln Ala Leu Ala Ala Gln Gly Ile Gly Thr Val Val Glu Leu
         2355                2360                2365
Gly Pro Asp Gly Thr Leu Ala Ala Leu Val Arg Glu Cys Ala Thr Glu
      2370                2375                2380
Ser Asp Arg Val Gly Arg Ile Ser Ser Ile Pro Leu Met Arg Arg Glu
   385                2390                2395                2400
Arg Asp Glu Thr Arg Ser Val Met Thr Ala Leu Ala His Leu His Thr
             2405                2410                2415
Arg Gly Gly Glu Val Asp Trp Gln Ala Phe Phe Ala Gly Thr Gly Ala
```

222

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         2420                 2425                 2430

Arg Gln Leu Glu Leu Pro Thr Tyr Ala Phe Gln Arg Gln His Tyr Trp
     2435                 2440                 2445

Ile Glu Ser Ser Ala Arg Pro Ala Arg Asp Arg Ala Asp Ile Gly Glu
   2450                 2455                 2460

Val Ala Glu Gln Phe Trp Thr Ala Val Asp Gln Gly Asp Leu Ala Thr
465                 2470                 2475                 2480

Leu Val Ala Ala Leu Asp Leu Gly Ala Asp Asp Asp Thr Cys Ala Ser
                 2485                 2490                 2495

Leu Ser Asp Val Leu Pro Ala Leu Ser Ser Trp Arg Ser Gly Leu Arg
                 2500                 2505                 2510

Asn Arg Ser Leu Val Asp Ser Cys Arg Tyr Arg Ile Ser Trp His Ser
     2515                 2520                 2525

Ser Arg Glu Val Pro Ala Pro Lys Ile Ser Gly Thr Trp Leu Leu Val
   2530                 2535                 2540

Val Pro Gly Ala Ala Asp Asp Gly Leu Val Thr Ala Leu Thr Ser Ser
545                 2550                 2555                 2560

Leu Val Gly Gly Gly Ala Glu Val Val Arg Ile Gly Leu Ser Glu Glu
                 2565                 2570                 2575

Asp Pro His Arg Glu Asp Val Ala Gln Arg Leu Ala Asn Ala Leu Thr
             2580                 2585                 2590

Asp Ala Gly Gln Leu Gly Gly Val Leu Ser Leu Leu Gly Leu Asp Glu
             2595                 2600                 2605

Ser Pro Ala Pro Gly Phe Ser Cys Leu Pro Thr Gly Phe Ala Leu Thr
   2610                 2615                 2620

Val Gln Leu Leu Arg Ala Leu Arg Lys Ala Asp Val Glu Ala Pro Phe
625                 2630                 2635                 2640

Trp Ala Val Thr Arg Gly Gly Val Ala Leu Glu Asp Val Arg Val Ser
         2645                 2650                 2655

Pro Glu Gln Ala Leu Val Trp Gly Leu Leu Arg Val Ala Gly Leu Glu
             2660                 2665                 2670

His Pro Glu Phe Trp Gly Gly Leu Ile Asp Leu Pro Ser Asp Trp Asp
```

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        2675              2680              2685

Asp Arg Leu Gly Ala Arg Leu Ala Gly Val Leu Ala Asp Gly Gly Glu
    2690              2695             2700

Asp Gln Val Ala Ile Arg Arg Gly Gly Val Phe Val Arg Arg Leu Glu
705              2710              2715              2720

Arg Ala Gly Ala Ser Gly Ala Gly Ser Val Trp Arg Pro Arg Gly Thr
            2725              2730              2735

Val Leu Val Thr Gly Gly Thr Gly Gly Leu Gly Ala His Val Ala Arg
        2740              2745              2750

Trp Leu Ala Gly Ala Gly Ala Glu His Val Val Leu Thr Ser Arg Arg
        2755              2760              2765

Gly Ala Asp Ala Pro Gly Ala Gly Glu Leu Arg Ala Glu Leu Glu Ala
    2770              2775              2780

Leu Gly Ala Arg Val Ser Ile Val Pro Cys Asp Val Ala Asp Arg Asp
785              2790              2795              2800

Ala Val Ala Gly Val Leu Ala Gly Ile Gly Gly Glu Cys Pro Leu Thr
            2805              2810              2815

Ala Val Val His Ala Ala Gly Val Gly Glu Ala Gly Asp Val Val Glu
        2820              2825              2830

Met Gly Leu Ala Asp Phe Ala Ala Val Leu Ser Ala Lys Val Arg Gly
        2835              2840              2845

Ala Ala Asn Leu Asp Glu Leu Leu Ala Asp Ser Glu Leu Asp Ala Phe
    2850              2855              2860

Val Met Phe Ser Ser Val Ser Gly Val Trp Gly Ala Gly Gly Gln Gly
865              2870              2875              2880

Ala Tyr Ala Ala Ala Asn Ala Tyr Leu Asp Ala Leu Ala Glu Gln Arg
            2885              2890              2895

Arg Ala Arg Gly Leu Val Gly Thr Ala Val Ala Trp Gly Pro Trp Ala
            2900              2905              2910

Gly Asp Gly Met Ala Ala Gly Glu Thr Gly Ala Gln Leu His Arg Met
        2915              2920              2925

Gly Leu Ala Ser Met Glu Pro Ser Ala Ala Leu Leu Ala Leu Gln Gly
```

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        2930                2935                2940

Ala Leu Asp Arg Asp Glu Thr Ser Leu Val Val Ala Asp Val Asp Trp
945                 2950                2955                2960

Ala Arg Phe Ala Pro Ala Phe Thr Ser Ala Arg Arg Arg Pro Leu Leu
             2965                2970                2975

Asp Thr Ile Asp Glu Ala Arg Ala Ala Leu Glu Thr Thr Gly Glu Gln
         2980                2985                2990

Ala Gly Thr Gly Lys Pro Val Glu Leu Thr Gln Arg Leu Ala Gly Leu
         2995                3000                3005

Ser Arg Lys Glu Arg Asp Asp Ala Val Leu Asp Leu Val Arg Ala Glu
         3010                3015                3020

Thr Ala Ala Val Leu Gly Arg Asp Asp Ala Thr Ala Leu Ala Pro Ser
025                 3030                3035                3040

Arg Pro Phe Gln Glu Leu Gly Phe Asp Ser Leu Met Ala Val Glu Leu
             3045                3050                3055

Arg Asn Arg Leu Asn Thr Ala Thr Gly Ile Gln Leu Pro Ala Ser Thr
         3060                3065                3070

Ile Phe Asp Tyr Pro Asn Ala Glu Ser Leu Ser Arg His Leu Cys Ala
         3075                3080                3085

Glu Leu Phe Pro Thr Glu Thr Thr Val Asp Ser Ala Leu Ala Glu Leu
         3090                3095                3100

Asp Arg Ile Glu Gln Gln Leu Ser Met Leu Thr Gly Glu Ala Arg Ala
105                 3110                3115                3120

Arg Asp Arg Ile Ala Thr Arg Leu Arg Ala Leu His Glu Lys Trp Asn
             3125                3130                3135

Ser Ala Ala Glu Val Pro Thr Gly Ala Asp Val Leu Ser Thr Leu Asp
         3140                3145                3150

Ser Ala Thr His Asp Glu Ile Phe Glu Phe Ile Asp Asn Glu Leu Asp
         3155                3160                3165

Leu Ser
3170
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<210> 47
<211> 14775
<212> DNA
<213> Saccharopolyspora spinosa

<220>
<221> CDS
<222> (1)..(14772)
<223> ORF21; Polyketidsynthase


<400> 47
atg gcc aat gaa gaa aag ctc ttc ggc tat ctg aag aag gta act gcg    48
Met Ala Asn Glu Glu Lys Leu Phe Gly Tyr Leu Lys Lys Val Thr Ala
  1               5                  10                  15


gac ctg cat cag acc cgg cag cgc ctg ctc gcg gcc gag agc cgg agt    96
Asp Leu His Gln Thr Arg Gln Arg Leu Leu Ala Ala Glu Ser Arg Ser
                20                  25                  30


cag gag ccg atc gcg atc gtc tcg gcg agc tgc cga ctg ccc ggc ggc   144
Gln Glu Pro Ile Ala Ile Val Ser Ala Ser Cys Arg Leu Pro Gly Gly
            35                  40                  45


gtc gac tct ccc gaa gcg ctc tgg caa ctc gtg cgc act ggc acc gac   192
Val Asp Ser Pro Glu Ala Leu Trp Gln Leu Val Arg Thr Gly Thr Asp
        50                  55                  60


gcc atc tcg gag ttc ccc gcc gac cgg ggc tgg gat ctc ggc cgg ttg   240
Ala Ile Ser Glu Phe Pro Ala Asp Arg Gly Trp Asp Leu Gly Arg Leu
 65                  70                  75                  80


tac gat ccc gac ccg aac cac cag gga acg tcg tac acg cgg gcc ggc   288
Tyr Asp Pro Asp Pro Asn His Gln Gly Thr Ser Tyr Thr Arg Ala Gly
                85                  90                  95


ggt ttc ctc gca gga gcg ggc gat ttc gac ccc gcc atg ttc ggg att   336
Gly Phe Leu Ala Gly Ala Gly Asp Phe Asp Pro Ala Met Phe Gly Ile
               100                 105                 110


tcg ccg cgt gag gcg ttg gcg atg gac ccg cag caa cgg ttg ttg ctg   384
Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu
               115                 120                 125


gag ctg tcc tgg gag gcc ctc gaa cgg gcg ggc ata gac ccg aca tcc   432
Glu Leu Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Asp Pro Thr Ser
           130                 135                 140
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ctg cgc ggc agc aag acc ggt gtc ttc ggt ggt gtc acg ccc cag gag   480
Leu Arg Gly Ser Lys Thr Gly Val Phe Gly Gly Val Thr Pro Gln Glu
145   150   155   160

tac ggg ccg tcc ttg cag gag atg agc cga aac gct ggg ggt ttt gga   528
Tyr Gly Pro Ser Leu Gln Glu Met Ser Arg Asn Ala Gly Gly Phe Gly
                 165   170   175

ctc acc ggg cgg atg gtg agt gtg gcg tcg ggt cgg gtt gcg tat tcg   576
Leu Thr Gly Arg Met Val Ser Val Ala Ser Gly Arg Val Ala Tyr Ser
                 180   185   190

ttt ggt ttt gag ggt cct gcg gtg acg gtg gat acg gcg tgt tcg tcg   624
Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser
                 195   200   205

tcg ttg gtg gcc ctg cat ttg gcg tgt cag tcg ttg cgt tcc ggc gaa   672
Ser Leu Val Ala Leu His Leu Ala Cys Gln Ser Leu Arg Ser Gly Glu
            210   215   220

tgc gat ctc gcg ctg gcc ggc ggt gtg acg gtg atg gcg aca ccg gcg   720
Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ala Thr Pro Ala
225   230   235   240

acg ttc gtg gag ttc tcc cgt cag cgt ggt ttg gct ccg gac ggg cgg   768
Thr Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg
                 245   250   255

tgc aag tcg ttc gcg gct gcc gcg gat ggc acc ggg tgg ggt gag ggt   816
Cys Lys Ser Phe Ala Ala Ala Ala Asp Gly Thr Gly Trp Gly Glu Gly
                 260   265   270

gcc ggt ctg gtg ttg ctg gag cgg ttg tcg gat gcg cgg cgg aat ggg   864
Ala Gly Leu Val Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly
            275   280   285

cac gag gtt ctg gcg gtg gtg cgg ggt agc gcg gtg aac cag gac ggc   912
His Glu Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly
            290   295   300

gcg tcg aat ggt ttg act gcg ccg aat ggt ccg tcg cag cag cgg gtg   960
Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln Arg Val
305   310   315   320

atc acc cag gcg ttg gcg agt gcg ggg ctg tcg gtt tcc gat gtg gat   1008
Ile Thr Gln Ala Leu Ala Ser Ala Gly Leu Ser Val Ser Asp Val Asp
                 325   330   335

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gcg gtc gag gca cat ggg acc ggg acc acg ttg ggt gat ccg atc gag    1056
Ala Val Glu Ala His Gly Thr Gly Thr Thr Leu Gly Asp Pro Ile Glu
            340             345             350

gca cag gcc ctg atc gcc acg tac ggg cag ggc cgg gag aag gat cgg    1104
Ala Gln Ala Leu Ile Ala Thr Tyr Gly Gln Gly Arg Glu Lys Asp Arg
            355             360             365

ccg ttg tgg ttg ggg tcg gtc aag tcc aac atc ggt cac acg cag gcg    1152
Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile Gly His Thr Gln Ala
            370             375             380

gcc gct ggc gtt gcc ggc gtc atc aag atg gtc ttg gcg atg cgg cac    1200
Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met Arg His
385             390             395             400

ggg cag ctg ccc gcc acg ttg cat gtg gat gag ccc acg tcg gcg gtg    1248
Gly Gln Leu Pro Ala Thr Leu His Val Asp Glu Pro Thr Ser Ala Val
            405             410             415

gac tgg tcg gcg ggt tcg gtc cgg ctt ctc acg gag aac acg ccc tgg    1296
Asp Trp Ser Ala Gly Ser Val Arg Leu Leu Thr Glu Asn Thr Pro Trp
            420             425             430

ccg gac agt ggt cgt cct tgc cgg gtg ggg gtg tcg tcg ttc ggg atc    1344
Pro Asp Ser Gly Arg Pro Cys Arg Val Gly Val Ser Ser Phe Gly Ile
            435             440             445

agc ggc acc aac gca cat gtg att ctc gaa cag tct cca gtc gag cag    1392
Ser Gly Thr Asn Ala His Val Ile Leu Glu Gln Ser Pro Val Glu Gln
            450             455             460

ggc gaa ccg gcc ggg ccg gtc gaa ggc gag cgg gaa ccg gat gta gcc    1440
Gly Glu Pro Ala Gly Pro Val Glu Gly Glu Arg Glu Pro Asp Val Ala
465             470             475             480

gtc ccc gtg gtg cct tgg gtg ctg tcg ggt aag aca ccg gag gct gcg    1488
Val Pro Val Val Pro Trp Val Leu Ser Gly Lys Thr Pro Glu Ala Ala
            485             490             495

cgg gcg cag gcc gaa cgg gtg cat tcg cat atc gag gac cgg ccg ggg    1536
Arg Ala Gln Ala Glu Arg Val His Ser His Ile Glu Asp Arg Pro Gly
            500             505             510

ctg tcg ccg gtg gat gtg gcg tat tcg cta gga atg aca cgc gcg gcg    1584
Leu Ser Pro Val Asp Val Ala Tyr Ser Leu Gly Met Thr Arg Ala Ala
            515             520             525
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228

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ctg gat gaa cgc gca gtg gtg ttg ggc tcg gac cgt gcc gcg ctc ctg   1632
Leu Asp Glu Arg Ala Val Val Leu Gly Ser Asp Arg Ala Ala Leu Leu
    530             535             540

acc ggg ttg agg gca ttc gcc gac ggc tgc gat gcg ccc gaa gtg gtt   1680
Thr Gly Leu Arg Ala Phe Ala Asp Gly Cys Asp Ala Pro Glu Val Val
545             550             555             560

tcg ggg tct gtg ggg ctt ggt ggc cgc gtc ggg ttc gtg ttc tcg ggt   1728
Ser Gly Ser Val Gly Leu Gly Gly Arg Val Gly Phe Val Phe Ser Gly
                565             570             575

cag ggt ggt cag tgg ccg ggg atg ggc cgg ggg ctc tac tcg gtg ttt   1776
Gln Gly Gly Gln Trp Pro Gly Met Gly Arg Gly Leu Tyr Ser Val Phe
                580             585             590

ccg gtg ttc gcc gac gcg ttc gac gag gct tgc gcg gag ttg gat gca   1824
Pro Val Phe Ala Asp Ala Phe Asp Glu Ala Cys Ala Glu Leu Asp Ala
            595             600             605

cac ctg ggc cag gaa ctg cgg gtt cgg gat gtg gtg ttc ggt tcg caa   1872
His Leu Gly Gln Glu Leu Arg Val Arg Asp Val Val Phe Gly Ser Gln
    610             615             620

gcg tgg ttg ctg gat cgg acg gtg tgg gcg cag tcg ggt ttg ttc gcg   1920
Ala Trp Leu Leu Asp Arg Thr Val Trp Ala Gln Ser Gly Leu Phe Ala
625             630             635             640

ttg cag att ggc ttg ctg cgg ctg ctg ggt tcg tgg ggt gtt cgg ccg   1968
Leu Gln Ile Gly Leu Leu Arg Leu Leu Gly Ser Trp Gly Val Arg Pro
                645             650             655

gat gtg gtg ttg ggg cac tcg gtg ggt gag ctg gct gcg gtg cat gcg   2016
Asp Val Val Leu Gly His Ser Val Gly Glu Leu Ala Ala Val His Ala
                660             665             670

gct ggt gtg ttg tcg ttg tcg gag gcc gcg cgg ttg gtg gcg ggt cgc   2064
Ala Gly Val Leu Ser Leu Ser Glu Ala Ala Arg Leu Val Ala Gly Arg
                675             680             685

gcc cgg ttg atg cag gcg ttg cct tct ggt ggt gcc atg ctc gcg gtc   2112
Ala Arg Leu Met Gln Ala Leu Pro Ser Gly Gly Ala Met Leu Ala Val
    690             695             700

gct acg ggt gag ttt cag gtc gat cct ctg ctg gat ggg gtg cgg gac   2160
Ala Thr Gly Glu Phe Gln Val Asp Pro Leu Leu Asp Gly Val Arg Asp
705             710             715             720
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cgg atc ggt atc gcg gcg gtg aat ggc ccg gaa tcg gtt gtg ctc tct   2208
Arg Ile Gly Ile Ala Ala Val Asn Gly Pro Glu Ser Val Val Leu Ser
            725   730   735

ggt gac cgc gag ctg ctc acc gag atc gct gat cgg ttg cac gat cag   2256
Gly Asp Arg Glu Leu Leu Thr Glu Ile Ala Asp Arg Leu His Asp Gln
            740   745   750

ggg tgc cgg acc cgg tgg ttg cgg gtg tcg cat gct ttc cat tcg ccc   2304
Gly Cys Arg Thr Arg Trp Leu Arg Val Ser His Ala Phe His Ser Pro
            755   760   765

cat atg gag ccg atg ctg gag gag ttc gcc cag atc tcc cga ggc cgc   2352
His Met Glu Pro Met Leu Glu Glu Phe Ala Gln Ile Ser Arg Gly Arg
    770   775   780

gaa tat cac gca ccg gaa ctg ccg atc atc tcg acc ctg atc ggt gag   2400
Glu Tyr His Ala Pro Glu Leu Pro Ile Ile Ser Thr Leu Ile Gly Glu
785   790   795   800

ctg gac ggt ggt cga gtg atg ggc act ccc gag tac tgg gtg cgt cag   2448
Leu Asp Gly Gly Arg Val Met Gly Thr Pro Glu Tyr Trp Val Arg Gln
                805   810   815

gtg cgt gag ccc gtc cgt ttc gcc gag ggt gtc cag gcg ctt gtc ggt   2496
Val Arg Glu Pro Val Arg Phe Ala Glu Gly Val Gln Ala Leu Val Gly
            820   825   830

cag ggt gtc ggc acg att gtc gaa ttg ggt ccg gac ggg gcg ttg tcg   2544
Gln Gly Val Gly Thr Ile Val Glu Leu Gly Pro Asp Gly Ala Leu Ser
            835   840   845

acg ttg gtc gag gag tgt gtg gcg gaa tcc ggg cgg gtg gcc ggg atc   2592
Thr Leu Val Glu Glu Cys Val Ala Glu Ser Gly Arg Val Ala Gly Ile
    850   855   860

ccg ctg atg cgc aag gac cgc gac gag gcg cga acc gtg ctg gca gct   2640
Pro Leu Met Arg Lys Asp Arg Asp Glu Ala Arg Thr Val Leu Ala Ala
865   870   875   880

ttg gcg cag atc cac acc cgt ggt ggt gag gtg gac tgg cgg tcg ttt   2688
Leu Ala Gln Ile His Thr Arg Gly Gly Glu Val Asp Trp Arg Ser Phe
                885   ·890   895

ttc gcc ggt acc ggg gcg aag caa gtc gac ctg ccc acc tac gcc ttc   2736
Phe Ala Gly Thr Gly Ala Lys Gln Val Asp Leu Pro Thr Tyr Ala Phe
                900   905   910

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cag cgg cag cgg tac tgg ctg gca tcc acc ggg cgt gcg ggt gac gtg    2784
Gln Arg Gln Arg Tyr Trp Leu Ala Ser Thr Gly Arg Ala Gly Asp Val
        915                 920                 925

acc gcc gcc gga ttg gcc gag gcg gac cat ccg ctg ctc ggt gcg gtg    2832
Thr Ala Ala Gly Leu Ala Glu Ala Asp His Pro Leu Leu Gly Ala Val
        930                 935                 940

gtt gcg ttg gca gac ggc gaa ggt gtg gtg ctg acc ggt cgg ttg aca    2880
Val Ala Leu Ala Asp Gly Glu Gly Val Val Leu Thr Gly Arg Leu Thr
945                 950                 955                 960

gcg ggt tcg cat ccg tgg ttg tcc gat cac cgg gtg ctg ggc gaa atc    2928
Ala Gly Ser His Pro Trp Leu Ser Asp His Arg Val Leu Gly Glu Ile
                965                 970                 975

gtc gtc ccc ggc acc gcg atc gtc gag ctg gtg tgg cac gtc ggc gag    2976
Val Val Pro Gly Thr Ala Ile Val Glu Leu Val Trp His Val Gly Glu
                980                 985                 990

cgc ctc ggt tgt ggc cgg gtg gaa gaa ctg gct ttg gaa gcg ccc ctg    3024
Arg Leu Gly Cys Gly Arg Val Glu Glu Leu Ala Leu Glu Ala Pro Leu
                995                 1000                1005

atc ctg ccg gat cat gga gcg gtc cag gtt cag gtg ctg gtg gga ccg    3072
Ile Leu Pro Asp His Gly Ala Val Gln Val Gln Val Leu Val Gly Pro
    1010                1015                1020

ccc ggg gaa tcc gga gcc cgg tcg gtg gcg ctc tac tcc tgt cct ggc    3120
Pro Gly Glu Ser Gly Ala Arg Ser Val Ala Leu Tyr Ser Cys Pro Gly
1025                1030                1035                1040

gag gcg atc gaa ccc gag tgg aag aag cac gcg acg ggc gtg ctt ctc    3168
Glu Ala Ile Glu Pro Glu Trp Lys Lys His Ala Thr Gly Val Leu Leu
                1045                1050                1055

cca ccc gtg gcc gcc gag aac cat gag ctg acc gca tgg ccc ccg gag    3216
Pro Pro Val Ala Ala Glu Asn His Glu Leu Thr Ala Trp Pro Pro Glu
                1060                1065                1070

aat gcg acc gaa atc gat gca gac ggg gtc tac gca ttc ctt gaa ggg    3264
Asn Ala Thr Glu Ile Asp Ala Asp Gly Val Tyr Ala Phe Leu Glu Gly
        1075                1080                1085

cac ggt ttc gcg tac gga ccg gcc ttt aga tgt ctg cgc ggt gcc tgg    3312
His Gly Phe Ala Tyr Gly Pro Ala Phe Arg Cys Leu Arg Gly Ala Trp
    1090                1095                1100
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cga cga ggc ggg gag gtg ttc gcc gaa gtc gca ttg ccg gat gac atg    3360
Arg Arg Gly Gly Glu Val Phe Ala Glu Val Ala Leu Pro Asp Asp Met
1105          1110          1115          1120


cag gcg ggg gtc gat cga ttc ggc gtc cac ccc gcg ttg ctg gac gcg    3408
Gln Ala Gly Val Asp Arg Phe Gly Val His Pro Ala Leu Leu Asp Ala
              1125          1130          1135


gtt ctg cat gcc gcc gca gcc gag acg tcg gtg gtc cag agc gaa gcg    3456
Val Leu His Ala Ala Ala Ala Glu Thr Ser Val Val Gln Ser Glu Ala
              1140          1145          1150


cgg gtg ccg ttc tcg tgg cgt ggg gtg gaa ctt cgc gcc act gaa agc    3504
Arg Val Pro Phe Ser Trp Arg Gly Val Glu Leu Arg Ala Thr Glu Ser
              1155          1160          1165


gcg gtg gtg cgg gcg cgc ctc tcg ttg act tcg gat gac gaa ctg tcg    3552
Ala Val Val Arg Ala Arg Leu Ser Leu Thr Ser Asp Asp Glu Leu Ser
      1170          1175          1180


ttg gtc gca gtg gac ccg gct ggc cga ttc gtg gcc acg gtt gat tcg    3600
Leu Val Ala Val Asp Pro Ala Gly Arg Phe Val Ala Thr Val Asp Ser
1185          1190          1195          1200


ctg gtg acc cga ccg atc tcc cgg cag cag gtg agg tct ggc gcg atc    3648
Leu Val Thr Arg Pro Ile Ser Arg Gln Gln Val Arg Ser Gly Ala Ile
              1205          1210          1215


ggt gat tgc ctg ttc gag gtg gag tgg cac cgg aag gcg ttg ttg gga    3696
Gly Asp Cys Leu Phe Glu Val Glu Trp His Arg Lys Ala Leu Leu Gly
              1220          1225          1230


aca acc gcc ggc gac gac ctt gcc atc gtc ggt gac ggt ccc agt tgg    3744
Thr Thr Ala Gly Asp Asp Leu Ala Ile Val Gly Asp Gly Pro Ser Trp
              1235          1240          1245


ccg gaa tcg gtg cgc gca acc gca cgg ttc gcg acc ctg gat gag ttc    3792
Pro Glu Ser Val Arg Ala Thr Ala Arg Phe Ala Thr Leu Asp Glu Phe
      1250          1255          1260


cgt gcg gcc gtg gac tcg gac gtt cct gcc ccg ggt tcg gtg ttg gtc    3840
Arg Ala Ala Val Asp Ser Asp Val Pro Ala Pro Gly Ser Val Leu Val
1265          1270          1275          1280


gca gct atg tcg gcc gaa gag gtc gag ggt gga tcc ctg ccg tcg cgc    3888
Ala Ala Met Ser Ala Glu Glu Val Glu Gly Gly Ser Leu Pro Ser Arg
              1285          1290          1295
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gcc caa gag tcg acc tcc gat ctg ctg gct ctc gtg cag tcg tgg ctt    3936
Ala Gln Glu Ser Thr Ser Asp Leu Leu Ala Leu Val Gln Ser Trp Leu
        1300            1305            1310

gcg gac gag cgg ttc gcc gaa tcc cag ctc gtg gtc gtc acg cgt gca    3984
Ala Asp Glu Arg Phe Ala Glu Ser Gln Leu Val Val Val Thr Arg Ala
        1315            1320            1325

gcg gtg tcg gcc gac tcg gat tcg gac gtc gcg gac ctg gtg ggt gcg    4032
Ala Val Ser Ala Asp Ser Asp Ser Asp Val Ala Asp Leu Val Gly Ala
        1330            1335            1340

tcg tcg tgg ggg ttg ttg agt tca gcc cag tcg gag aac ccg ggt cgc    4080
Ser Ser Trp Gly Leu Leu Ser Ser Ala Gln Ser Glu Asn Pro Gly Arg
1345            1350            1355            1360

ttc gtg ctg gtg gac gtg gac ggc aca cct gag tcg tgg cag gcg ttg    4128
Phe Val Leu Val Asp Val Asp Gly Thr Pro Glu Ser Trp Gln Ala Leu
            1365            1370            1375

ccg gcc gcc gtg cga gca gga gaa ccg cag ctg gca ctt cgg cgc ggc    4176
Pro Ala Ala Val Arg Ala Gly Glu Pro Gln Leu Ala Leu Arg Arg Gly
        1380            1385            1390

gtg gcg ctg gtg cct cgg ttg gcg cga ctc acg gtg cgc gag gag ggc    4224
Val Ala Leu Val Pro Arg Leu Ala Arg Leu Thr Val Arg Glu Glu Gly
        1395            1400            1405

tcc tcc ccg caa ctc gac acg gac ggg acc gtc ctc atc acg ggt ggc    4272
Ser Ser Pro Gln Leu Asp Thr Asp Gly Thr Val Leu Ile Thr Gly Gly
    1410            1415            1420

acc ggt gcg ttg ggg gga gtg gtt gcc cgt cac ctg gtg gag gag cac    4320
Thr Gly Ala Leu Gly Gly Val Val Ala Arg His Leu Val Glu Glu His
1425            1430            1435            1440

ggg att cgg cgt ttg gtg ttg gca ggc cgg cgt ggc tgg aat gcg cct    4368
Gly Ile Arg Arg Leu Val Leu Ala Gly Arg Arg Gly Trp Asn Ala Pro
            1445            1450            1455

gga gtc cac gag ttg gtg gat gag ctg gcg cgc gcg ggc gcc gtg gtt    4416
Gly Val His Glu Leu Val Asp Glu Leu Ala Arg Ala Gly Ala Val Val
            1460            1465            1470

gag gtg gtg gct tgc gat gtg gct gac cgc acc gat ctg gag cac gtg    4464
Glu Val Val Ala Cys Asp Val Ala Asp Arg Thr Asp Leu Glu His Val
        1475            1480            1485
```

233

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ctg gcc gcc att ccg gtc gac tgg ccg ctg cgg ggg atc gtg cat acc    4512
Leu Ala Ala Ile Pro Val Asp Trp Pro Leu Arg Gly Ile Val His Thr
    1490             1495             1500


gct ggg gtg ctg gcc gac gga gtg atc ggg tcc ttg tcg gcg gcg gat    ·4560  ·.
Ala Gly Val Leu Ala Asp Gly Val Ile Gly Ser Leu Ser Ala Ala Asp
1505 ·           1510             1515             · 1520


gtg ggc acg gtg ttt gcc ccg aag gtg acg ggg gca tgg cat ctg cac    4608
Val Gly Thr Val Phe Ala Pro Lys Val Thr Gly Ala Trp His Leu His
            1525             1530             1535


gag ttg acc cgc gat ctg gat ctg tcg ttc ttc gtt ctt ttc tct tcc    4656
Glu Leu Thr Arg Asp Leu Asp Leu Ser Phe Phe Val Leu Phe Ser Ser
        1540             1545             1550          ·


ttc tcc ggg att gcg ggt gcc gca ggg cag gcc aac tac gcg gcg gcg    4704
Phe Ser Gly Ile Ala Gly Ala Ala Gly Gln Ala Asn Tyr Ala Ala Ala
        1555      ·        1560             1565   .


aac acg ttc ctg gat gca ttg gcg cgt tat cgc cgg gcg cgt ggg ctg    4752
Asn Thr Phe Leu Asp Ala Leu Ala Arg Tyr Arg Arg Ala Arg Gly Leu
    1570             1575             1580


cct ggg ttg tcg ttg gcg tgg gga ctg tgg gcg caa ccc agc ggt atg    4800
Pro Gly Leu Ser Leu Ala Trp Gly Leu Trp Ala Gln Pro Ser Gly Met
1585             1590             1595             1600


acg agt ggc ttg gac gcg gcg tcg gtg gag cgg ttg gcg cgg acg ggc    4848
Thr Ser Gly Leu Asp Ala Ala Ser Val Glu Arg Leu Ala Arg Thr Gly
    ·        1605             1610             1615


atc gca gaa ctt tcc acg gag gat gga ctc cgc ctg ttc gat gcc gcg    4896
Ile Ala Glu Leu Ser Thr Glu Asp Gly Leu Arg Leu Phe Asp Ala Ala
            1620             1625             1630
        ·


ttc gcg aag gac cgg gct tgc gtc gtt gcc gct cga ttg gac agg gcg    4944
Phe Ala Lys Asp Arg Ala Cys Val Val Ala Ala Arg Leu Asp Arg Ala
        1635             1640             1645


ctg ctg gtc ggg aac gga cga tcg cac gcg att ccg gcg ctg ttg agc    4992
Leu Leu Val Gly Asn Gly Arg Ser His Ala Ile Pro Ala Leu Leu Ser
    1650             1655             1660


gcg ttg gtt cct gtt cgc ggc ggt gtg gcg agg aaa aca gcc aat tct    5040
Ala Leu Val Pro Val Arg Gly Gly Val Ala Arg Lys Thr Ala Asn Ser
1665             1670             1675          · 1680
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234 .

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cag gcc gcg gat gag gac gca ctg ttg ggt ttg gtg cgg gag cac gtt   5088
Gln Ala Ala Asp Glu Asp Ala Leu Leu Gly Leu Val Arg Glu His Val
              1685            1690            1695

tcg gcc gtg ctg ggt tat tcg ggt gcg gtc gag gtt ggg ggc gac cgt   5136
Ser Ala Val Leu Gly Tyr Ser Gly Ala Val Glu Val Gly Gly Asp Arg
              1700            1705            1710

gct ttc cgt gat ctg ggt ttt gat tcg ttg tct ggc gtg gag ttg cgg   5184
Ala Phe Arg Asp Leu Gly Phe Asp Ser Leu Ser Gly Val Glu Leu Arg
              1715            1720            1725

aac cgc ctt gcc ggg gtg ctg ggg gtg cgg ttg ccg gcg act gcg gtg   5232
Asn Arg Leu Ala Gly Val Leu Gly Val Arg Leu Pro Ala Thr Ala Val
         1730            1735            1740

ttc gac tat ccg acg ccg cgg gcg ctg gcg cgt ttc ctg cat cag gaa   5280
Phe Asp Tyr Pro Thr Pro Arg Ala Leu Ala Arg Phe Leu His Gln Glu
1745            1750            1755            1760

ctg gca ggc gag gtc gcg tcc acg tcg acg ccg gtg acc agg gca gcg   5328
Leu Ala Gly Glu Val Ala Ser Thr Ser Thr Pro Val Thr Arg Ala Ala
              1765            1770            1775

agt gcc gaa gag gat ctt gtt gcg att gtc ggg atg gga tgt cgt ttt   5376
Ser Ala Glu Glu Asp Leu Val Ala Ile Val Gly Met Gly Cys Arg Phe
              1780            1785            1790

ccg ggt ggg gtg tcg tcg ccg gag gag ctt tgg cgg ctg gtg gcc ggc   5424
Pro Gly Gly Val Ser Ser Pro Glu Glu Leu Trp Arg Leu Val Ala Gly
              1795            1800            1805

ggc gtg gat gcg gtg gct ggg ttc cca gac gat cgc ggc tgg gat ctc   5472
Gly Val Asp Ala Val Ala Gly Phe Pro Asp Asp Arg Gly Trp Asp Leu
         1810            1815            1820

gcg gcg ttg tac gat cct gat ccc gat cgt ctc ggg acc tcg tat gtg   5520
Ala Ala Leu Tyr Asp Pro Asp Pro Asp Arg Leu Gly Thr Ser Tyr Val
1825            1830            1835            1840

tgt gag ggc ggg ttt ctg cgg gac gcg gcg gag ttc gat gct gac atg   5568
Cys Glu Gly Gly Phe Leu Arg Asp Ala Ala Glu Phe Asp Ala Asp Met
              1845            1850            1855

ttc ggc atc agc ccg cgt gag gcg ttg gcg atg gat ccg cag cag cgg   5616
Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg
         1860            1865            1870
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ttg ctg ctg gag gtc·gcc tgg gaa acc ttg gag cgg gct ggg atc gat   5664
Leu Leu Leu Glu Val Ala Trp Glu Thr Leu Glu Arg Ala Gly Ile Asp
        1875   1880   1885

ccg ttc tcg ttg cac ggc agc cgg acc ggt gtg ttc gcg ggc ttg atg   5712
Pro Phe Ser Leu His Gly Ser Arg Thr Gly Val Phe Ala Gly Leu Met
        1890   1895   1900

tac cac gac tat ggg gcc cga ttc att acc aga gca ccg gag ggc ttc   5760
Tyr His Asp Tyr Gly Ala Arg Phe Ile Thr Arg Ala Pro Glu Gly Phe
1905   1910   1915   1920

gaa ggg cac ctc ggg acg ggc aat gcg ggg agc gtg ctg tcg ggt cgg   5808
Glu Gly His Leu Gly Thr Gly Asn Ala Gly Ser Val Leu Ser Gly Arg
                1925   1930   1935

gtt gcg tat tcg ttt ggt ttc gag ggt cct gcg gtg acg gtg gat acg   5856
Val Ala Tyr Ser Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr
                1940   1945   1950

gcg tgt tcg tcg tcg ttg gtg gcg tta cac ctg gcg ggt caa gca ctg   5904
Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala Gly Gln Ala Leu
        1955   1960   1965

cgg gcc ggt gag tgc gaa ttc gcc ctt gcc ggt ggc gtc acg gtg atg   5952
Arg Ala Gly Glu Cys Glu Phe Ala Leu Ala Gly Gly Val Thr Val Met
        1970   1975   1980

tcg acg ccg acg acg ttc gtg gag ttc tcc cgt caa cgg ggt ctg gct   6000
Ser Thr Pro Thr Thr Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala
1985   1990   1995   2000

ccg gat ggg cgg tgc aag tcg ttc gcg gcg gcc gcg gat ggc acc ggg   6048
Pro Asp Gly Arg Cys Lys Ser Phe Ala Ala Ala Ala Asp Gly Thr Gly
                2005   2010   2015

tgg ggc gag ggt gcc ggt ctg gtg ttg ctg gag cgg ttg tcg gat gcc   6096
Trp Gly Glu Gly Ala Gly Leu Val Leu Leu Glu Arg Leu Ser Asp Ala
                2020   2025   2030

cgg cgc aat ggg cac gag gtt ctg gcg gtg gtg cgg ggt agc gcg gtg   6144
Arg Arg Asn Gly His Glu Val Leu Ala Val Val Arg Gly Ser Ala Val
        2035   2040   2045

aac cag gac ggc gcg tcg aat ggc ttg act gcg cca aat ggt ccg tca   6192
Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser
        2050   2055   2060

236

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cag caa agg gtg atc acc cag gca ctc acg agt gcc ggg ctg tcc gtg    6240
Gln Gln Arg Val Ile Thr Gln Ala Leu Thr Ser Ala Gly Leu Ser Val
2065            2070            2075            2080


tcc gac gtg gat gct gtg gag gcg cat ggg acg ggc acg cgg ctt ggt    6288
Ser Asp Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly
            2085            2090            2095


gat ccg atc gag gcg cag gcg ttg atc gct acg tac ggc cgg gat cgt    6336
Asp Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr Tyr Gly Arg Asp Arg
        2100            2105            2110


gat ccc ggt cgg ccg ttg tgg ctg ggg tcg gtg aag tcg aat att ggt    6384
Asp Pro Gly Arg Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile Gly
        2115            2120            2125


cac acc cag gcg gcg gcg ggt gtc gct ggt gtg atc aag atg gtg atg    6432
His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Met
    2130            2135            2140


gcg atg cgg cag ggg gag ctg ccg cgc acg ttg cac gtg gac gag ccc    6480
Ala Met Arg Gln Gly Glu Leu Pro Arg Thr Leu His Val Asp Glu Pro
2145            2150            2155            2160


tcc gcg cag gtg gac tgg tct gcg ggc acg gtc caa ctc ctc acg gag    6528
Ser Ala Gln Val Asp Trp Ser Ala Gly Thr Val Gln Leu Leu Thr Glu
            2165            2170            2175


aac acg ccc tgg ccc gac agc ggt cgt ctt cgc cgg gcg ggc gtg tca    6576
Asn Thr Pro Trp Pro Asp Ser Gly Arg Leu Arg Arg Ala Gly Val Ser
            2180            2185            2190


tcg ttc ggg atc agt ggc acc aac gcg cac ctg atc ctt gaa caa cct    6624
Ser Phe Gly Ile Ser Gly Thr Asn Ala His Leu Ile Leu Glu Gln Pro
        2195            2200            2205


ccg cga gag tcg cag cgc tca aca gag ccg gat tcg ggt tct gtc cgc    6672
Pro Arg Glu Ser Gln Arg Ser Thr Glu Pro Asp Ser Gly Ser Val Arg
    2210            2215            2220


gat ttt ccg gtg gtg ccg tgg atg gtg tcg ggc aaa aca ccc gaa gcg    6720
Asp Phe Pro Val Val Pro Trp Met Val Ser Gly Lys Thr Pro Glu Ala
2225            2230            2235            2240


cta tcc gcc cag gca gat gca ttg atg tcc tac ttg agc aat cgc gtt    6768
Leu Ser Ala Gln Ala Asp Ala Leu Met Ser Tyr Leu Ser Asn Arg Val
        2245            2250            2255
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237

gat gct tcc ccg cga gat atc ggt tat tcg ctt gcg gtg acc cgt ccg   6816
Asp Ala Ser Pro Arg Asp Ile Gly Tyr Ser Leu Ala Val Thr Arg Pro
            2260   2265   2270

gcg ttg gac cac cgc gct gtc gtg ctg ggt gcg gat cgt gcc gcg ttg   6864
Ala Leu Asp His Arg Ala Val Val Leu Gly Ala Asp Arg Ala Ala Leu
            2275   2280   2285

ctg ccg ggc ttg aaa gcg ctg gcc gtt agt aat gac gct gcc gag gtg   6912
Leu Pro Gly Leu Lys Ala Leu Ala Val Ser Asn Asp Ala Ala Glu Val
            2290   2295   2300

atc acc ggc act cgt gcc gct ggg ccg gtc gga ttc gtg ttc tcc ggt   6960
Ile Thr Gly Thr Arg Ala Ala Gly Pro Val Gly Phe Val Phe Ser Gly
2305   2310   2315   2320

caa ggt ggt cag tgg ccc ggg atg gga agc ggg ctc cac tcg gcg ttt   7008
Gln Gly Gly Gln Trp Pro Gly Met Gly Ser Gly Leu His Ser Ala Phe
                2325   2330   2335

ccg gtg ttc gcc gac gcg ttt gac gaa gcc tgc tgc gag ctg gat gcg   7056
Pro Val Phe Ala Asp Ala Phe Asp Glu Ala Cys Cys Glu Leu Asp Ala
                2340   2345   2350

cat ctc ggg cag atg gcc cgg cta cga gat gtg ttg tcc ggt tcg gat   7104
His Leu Gly Gln Met Ala Arg Leu Arg Asp Val Leu Ser Gly Ser Asp
            2355   2360   2365

acg caa ctt ctg gac cag acc ttg tgg gcg cag ccg ggc ctg ttc gcg   7152
Thr Gln Leu Leu Asp Gln Thr Leu Trp Ala Gln Pro Gly Leu Phe Ala
            2370   2375   2380

ttg caa gtc gga ctc tgg gag ttg ttg ggt tcg tgg ggt gtc cgg ccc   7200
Leu Gln Val Gly Leu Trp Glu Leu Leu Gly Ser Trp Gly Val Arg Pro
2385   2390   2395   2400

gct gtg gtg ctg ggc cac tcg gtc ggt gag ctg gcg gcg gcg ttc gcg   7248
Ala Val Val Leu Gly His Ser Val Gly Glu Leu Ala Ala Ala Phe Ala
                2405   2410   2415

gct gga gtg ttg tcg ttg cgg gat gcg gct cgg ctg gtg gcg ggc cgt   7296
Ala Gly Val Leu Ser Leu Arg Asp Ala Ala Arg Leu Val Ala Gly Arg
            2420   2425   2430

gcc cgg ttg atg caa gcc ctg cca act ggc ggt gcc atg ctc gct gcg   7344
Ala Arg Leu Met Gln Ala Leu Pro Thr Gly Gly Ala Met Leu Ala Ala
            2435   2440   2445

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gct gct gga gag gag cag ctg cgc ccg ttg ctg gcc gac tgc ggt gat    7392
Ala Ala Gly Glu Glu Gln Leu Arg Pro Leu Leu Ala Asp Cys Gly Asp
   2450                2455                2460


cgt gtg ggg atc gcc gcg gtc aac gct ccc ggg tcg gtg gtg ctc tcc    7440
Arg Val Gly Ile Ala Ala Val Asn Ala Pro Gly Ser Val Val Leu Ser
2465                2470                2475                2480


ggt gat cgg gat gtg ctc gat gac att gcc ggt cgg ctg gac ggg caa    7488
Gly Asp Arg Asp Val Leu Asp Asp Ile Ala Gly Arg Leu Asp Gly Gln
                2485                2490                2495


ggg atc cgg tcc agg tgg ttg cgg gtt tcg cat gcg ttt cat tcg cat    7536
Gly Ile Arg Ser Arg Trp Leu Arg Val Ser His Ala Phe His Ser His
                2500                2505                2510


cgg atg gat ccg atg ctg gcg gag ttc acc gaa atc gcc cgg agc gtg    7584
Arg Met Asp Pro Met Leu Ala Glu Phe Thr Glu Ile Ala Arg Ser Val
        2515                2520                2525


gac tac cgg tcg tca ggg ctg ccg atc gtg tcg acg ttg acg ggt gag    7632
Asp Tyr Arg Ser Ser Gly Leu Pro Ile Val Ser Thr Leu Thr Gly Glu
        2530                2535                2540


ctc gat gag gtc ggc atg ccg gct acg ccg gag tat tgg gtg cgc cag    7680
Leu Asp Glu Val Gly Met Pro Ala Thr Pro Glu Tyr Trp Val Arg Gln
2545                2550                2555                2560


gtg cga gaa ccc gtc cgc ttc gcc gac ggt gtt gct gcg ctc gcg gct    7728
Val Arg Glu Pro Val Arg Phe Ala Asp Gly Val Ala Ala Leu Ala Ala
                2565                2570                2575


cac ggt gtg agc acc gtc gtc gag gtc ggt ccg gat ggg gtg ttg tcg    7776
His Gly Val Ser Thr Val Val Glu Val Gly Pro Asp Gly Val Leu Ser
                2580                2585                2590


gcg ctg gtg cag gag tgc gcg gcc gga tcc gat cag ggc gga cgg gtg    7824
Ala Leu Val Gln Glu Cys Ala Ala Gly Ser Asp Gln Gly Gly Arg Val
                2595                2600                2605


gcc gcg gtt ccg ctc atg cgc agc aat cgc gac gag gcg cac acg gtg    7872
Ala Ala Val Pro Leu Met Arg Ser Asn Arg Asp Glu Ala His Thr Val
   2610                2615                2620


aca acg gca ttg gcg cag atc cat gtg cgt ggt gct gag gtg gac tgg    7920
Thr Thr Ala Leu Ala Gln Ile His Val Arg Gly Ala Glu Val Asp Trp
2625                2630                2635                2640
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cgg tcg ttt ttc gcc ggt acc ggg gca aag cag gtc gag ctg ccc acg   7968
Arg Ser Phe Phe Ala Gly Thr Gly Ala Lys Gln Val Glu Leu Pro Thr
            2645   2650   2655

tat gcc ttc caa cga cag cgg tac tgg ctt gac tca cca tcc gaa ccg   8016
Tyr Ala Phe Gln Arg Gln Arg Tyr Trp Leu Asp Ser Pro Ser Glu Pro
            2660   2665   2670

gtc ggg caa tcc gcc gat ccc gcg cgc cag tcg ggc ttc tgg gaa ctc   8064
Val Gly Gln Ser Ala Asp Pro Ala Arg Gln Ser Gly Phe Trp Glu Leu
          2675   2680   2685

gtc gag cag gaa gat gtc agc gcg ctc agc gcc gct ctg cac att acc   8112
Val Glu Gln Glu Asp Val Ser Ala Leu Ser Ala Ala Leu His Ile Thr
        2690   2695   2700

ggc gat cac gac gtg cag gcg tcc ctg gaa tcg gtg gtt ccg gtc ctc   8160
Gly Asp His Asp Val Gln Ala Ser Leu Glu Ser Val Val Pro Val Leu
2705   2710   2715   2720

tcc tcc tgg cat cgc cgg atc cgc aac gaa tcc ctg gtg cac cag tgg   8208
Ser Ser Trp His Arg Arg Ile Arg Asn Glu Ser Leu Val His Gln Trp
            2725   2730   2735

cgg tac cgg att tcc tgg cat gag cgg gca gat ttg cca gac ccc tcg   8256
Arg Tyr Arg Ile Ser Trp His Glu Arg Ala Asp Leu Pro Asp Pro Ser
          2740   2745   2750

ttg tcg ggg aca tgg ctc gtc gtc gtg ccg gag ggg tgg tcg gcg agt   8304
Leu Ser Gly Thr Trp Leu Val Val Val Pro Glu Gly Trp Ser Ala Ser
          2755   2760   2765

cgg caa gtt ctg cgt ttc aac gag atg ttc gag gaa cgg ggt tgc ccg   8352
Arg Gln Val Leu Arg Phe Asn Glu Met Phe Glu Glu Arg Gly Cys Pro
        2770   2775   2780

gca gtt ctg ttc gag ctc gcc ggg cac gac gag gaa gcc ctg gcg caa   8400
Ala Val Leu Phe Glu Leu Ala Gly His Asp Glu Glu Ala Leu Ala Gln
2785   2790   2795   2800

cga ttc cgc tcg ttg cct gtt gcg tca ggg gga ata agc ggc gtg ttg   8448
Arg Phe Arg Ser Leu Pro Val Ala Ser Gly Gly Ile Ser Gly Val Leu
           2805   2810   2815

tcc ttg ctg gcg ctg gat gaa tcg ccg tcc tcg ccg aac gct gct ttg   8496
Ser Leu Leu Ala Leu Asp Glu Ser Pro Ser Ser Pro Asn Ala Ala Leu
          2820   2825   2830

ccg aat ggc gcg ctg aac tcg ttg gta ctg ctg cga gct ctg cgg gcc   8544
Pro Asn Gly Ala Leu Asn Ser Leu Val Leu Leu Arg Ala Leu Arg Ala
     2835   2840   2845

gcg gat gtg tcg gcg cca ttg tgg ttg gcg acg tgt ggt ggt gtc gcg   8592
Ala Asp Val Ser Ala Pro Leu Trp Leu Ala Thr Cys Gly Gly Val Ala
     2850   2855   2860

gtc ggg gat gtg ccg gtg aac ccg ggg cag gcg ctg gtg tgg gga ctg   8640
Val Gly Asp Val Pro Val Asn Pro Gly Gln Ala Leu Val Trp Gly Leu
2865   2870   2875   2880

ggt cgc gtc gtc ggt ctg gag cat ccg gcc tgg tgg ggt ggc ctg gtc   8688
Gly Arg Val Val Gly Leu Glu His Pro Ala Trp Trp Gly Gly Leu Val
        2885   2890   2895

gac gtg ccg tgc ttg ctc gat gag gac gct cga gaa cgc ttg tcg gtc   8736
Asp Val Pro Cys Leu Leu Asp Glu Asp Ala Arg Glu Arg Leu Ser Val
     2900   2905   2910

gtg ttg gca ggt ctt ggc gag gac gag atc gcg gta cgt ccc ggt ggt   8784
Val Leu Ala Gly Leu Gly Glu Asp Glu Ile Ala Val Arg Pro Gly Gly
     2915   2920   2925

gtg ttc gtg cgg cgg ttg gaa cgc gct ggt gcg gcg tcg ggt gcc ggg   8832
Val Phe Val Arg Arg Leu Glu Arg Ala Gly Ala Ala Ser Gly Ala Gly
     2930   2935   2940

tcg gtg tgg cgt cct cgg ggg acg gtg ttg gtg acg ggt ggt acg ggc   8880
Ser Val Trp Arg Pro Arg Gly Thr Val Leu Val Thr Gly Gly Thr Gly
2945   2950   2955   2960

ggt ttg ggg gcg cat gtt gcc cgg tgg ttg gcg ggt gcc ggg gct gag   8928
Gly Leu Gly Ala His Val Ala Arg Trp Leu Ala Gly Ala Gly Ala Glu
        2965   2970   2975

cat gtg gtg ttg acc agc cgt cga ggc gcg gcg gct ccg ggc gct gga   8976
His Val Val Leu Thr Ser Arg Arg Gly Ala Ala Ala Pro Gly Ala Gly
        2980   2985   2990

gat ttg cgg gcg gag ctg gag gcg ctg ggc gct cgg gtt tcg atc acg   9024
Asp Leu Arg Ala Glu Leu Glu Ala Leu Gly Ala Arg Val Ser Ile Thr
     2995   3000   3005

gcc tgc gac gtg gcc gat cgt gac gct ttg gcc gaa gtg ttg gcg acc   9072
Ala Cys Asp Val Ala Asp Arg Asp Ala Leu Ala Glu Val Leu Ala Thr
     3010   3015   3020

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att ccg gat gat tgc ccg ctg acc gcg gtg atg cat gcg gcg ggg gtc    9120
Ile Pro Asp Asp Cys Pro Leu Thr Ala Val Met His Ala Ala Gly Val
3025            3030            3035                3040


gtt gaa gtc ggc gac gtg gcg tcg atg tgt ttg acc gac ttc gtt ggg    9168
Val Glu Val Gly Asp Val Ala Ser Met Cys Leu Thr Asp Phe Val Gly
               3045            3050            3055


gtg ctg tcg gcg aag gca ggt ggt gcg gcg aat ctc gat gag ttg ctc    9216
Val Leu Ser Ala Lys Ala Gly Gly Ala Ala Asn Leu Asp Glu Leu Leu
               3060            3065            3070


gcc gat gtc gag ctg gat gcc ttc gtg ctg ttc tca tcc gtc tcg ggt    9264
Ala Asp Val Glu Leu Asp Ala Phe Val Leu Phe Ser Ser Val Ser Gly
        3075            3080            3085


gtg tgg ggt gct ggc ggg cag ggc gct tat gcg gcg gcg aat gcc tac    9312
Val Trp Gly Ala Gly Gly Gln Gly Ala Tyr Ala Ala Ala Asn Ala Tyr
    3090            3095                3100


ttg gat gcg ttg gcg cag cag cgt cgg gca agg ggg ttg gtg ggg act    9360
Leu Asp Ala Leu Ala Gln Gln Arg Arg Ala Arg Gly Leu Val Gly Thr
3105            3110            3115            3120


gcg gtt gcg tgg ggc ccg tgg gcc ggt gac gga atg gcc gca ggt gaa    9408
Ala Val Ala Trp Gly Pro Trp Ala Gly Asp Gly Met Ala Ala Gly Glu
               3125            3130            3135


ggc ggt gca cag ctg cgc cgg gcc ggc ctg gtg cca atg gct gcg gat    9456
Gly Gly Ala Gln Leu Arg Arg Ala Gly Leu Val Pro Met Ala Ala Asp
        3140            3145            3150


cgg gcg ttg ctg gca ctt cag ggc gca ttg gat cgt gac gag aca tcc    9504
Arg Ala Leu Leu Ala Leu Gln Gly Ala Leu Asp Arg Asp Glu Thr Ser
        3155            3160            3165


ctg gtc gtg gcc gat atg gcg tgg gag agg ttc gcc ccg gtg ttc gcc    9552
Leu Val Val Ala Asp Met Ala Trp Glu Arg Phe Ala Pro Val Phe Ala
    3170            3175            3180


atg tcc cgt cgg cgt ccg ctg ctc gac gag ctg ccc gaa gca cag cag    9600
Met Ser Arg Arg Arg Pro Leu Leu Asp Glu Leu Pro Glu Ala Gln Gln
3185            3190            3195            3200


gcg ttg gcg gat gcg gag aac acc act gat gct gcg gac tcg gcc gtc    9648
Ala Leu Ala Asp Ala Glu Asn Thr Thr Asp Ala Ala Asp Ser Ala Val
               3205            3210            3215
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ccg cta ccg cgg ctc gcg ggc atg gca gcc gcc gaa cgc cgc cgc gcg    9696
Pro Leu Pro Arg Leu Ala Gly Met Ala Ala Ala Glu Arg Arg Arg Ala
        3220            3225            3230

atg ctg gac ctg gtg ctg gcg gag gcc tcg att gtg ttg gga cac aac    9744
Met Leu Asp Leu Val Leu Ala Glu Ala Ser Ile Val Leu Gly His Asn
        3235            3240            3245

ggg tct gac cca gtt ggt ccc gac cgg gcg ttc cag gag ctc gga ttt    9792
Gly Ser Asp Pro Val Gly Pro Asp Arg Ala Phe Gln Glu Leu Gly Phe
        3250            3255            3260

gat tcg ctg atg gcc gtc gaa ctg cgc aac agg ttg ggc gag gca aca    9840
Asp Ser Leu Met Ala Val Glu Leu Arg Asn Arg Leu Gly Glu Ala Thr
3265            3270            3275            3280

gga ttg agt ctg ccg gcc acg ttg atc ttc gat tat ccg agc cca tcc    9888
Gly Leu Ser Leu Pro Ala Thr Leu Ile Phe Asp Tyr Pro Ser Pro Ser
            3285            3290            3295

gcg ctg gct gag cag ctg gtc ggc gag ctg gtg gga gcg cag ccc gcg    9936
Ala Leu Ala Glu Gln Leu Val Gly Glu Leu Val Gly Ala Gln Pro Ala
        3300            3305            3310

acc acc gtc gtg gcc ggg gcc gat cca gtg gat gat ccg gtt gtc gtg    9984
Thr Thr Val Val Ala Gly Ala Asp Pro Val Asp Asp Pro Val Val Val
        3315            3320            3325

gtc gcg atg gga tgc cgg tat ccg ggc gac gtc tgc tcg ccc gag gag    10032
Val Ala Met Gly Cys Arg Tyr Pro Gly Asp Val Cys Ser Pro Glu Glu
        3330            3335            3340

ctg tgg cag ctg gtt tct gcg gga cgt gat gcg gta tcg acg ttc ccc    10080
Leu Trp Gln Leu Val Ser Ala Gly Arg Asp Ala Val Ser Thr Phe Pro
3345            3350            3355            3360

gtc gat cgg ggt tgg gac tgc aac acg ttg ttc gac ccg gat ccg gat    10128
Val Asp Arg Gly Trp Asp Cys Asn Thr Leu Phe Asp Pro Asp Pro Asp
            3365            3370            3375

cgg gca ggc agt acc tat gtg cga gaa ggt gcc ttc ctg acc ggt gct    10176
Arg Ala Gly Ser Thr Tyr Val Arg Glu Gly Ala Phe Leu Thr Gly Ala
        3380            3385            3390

gat cgg ttc gac gcc ggg ttc ttc ggc atc agc cct cgc gag gcg cgc    10224
Asp Arg Phe Asp Ala Gly Phe Phe Gly Ile Ser Pro Arg Glu Ala Arg
        3395            3400            3405
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243

gca atg gat ccg cag cag agg ttg ttg ctc gaa gtg gcg tgg gag gtt   10272
Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Val Ala Trp Glu Val
    3410   3415   3420

ttc gaa cga gca gga atc gct ccg ctg tcg ttg cgg ggt agc agg acc   10320
Phe Glu Arg Ala Gly Ile Ala Pro Leu Ser Leu Arg Gly Ser Arg Thr
3425   3430   3435   3440

ggt gtg ttc gcg ggg acc aat ggg cag gac cac ggt gcg aaa gtg gct   10368
Gly Val Phe Ala Gly Thr Asn Gly Gln Asp His Gly Ala Lys Val Ala
                3445   3450   3455

gcc gcg ccg gag gcg gcg ggt cac ctc ctg acc gga aac gcc gcg agt   10416
Ala Ala Pro Glu Ala Ala Gly His Leu Leu Thr Gly Asn Ala Ala Ser
            3460   3465   3470

gtc ctg gcc ggc cgg ctt tcc tac acg ttc ggc ctt gag ggg cct gcg   10464
Val Leu Ala Gly Arg Leu Ser Tyr Thr Phe Gly Leu Glu Gly Pro Ala
        3475   3480   3485

gtg gcg gtg gat acc gcg tgt tcg tcg tcg ttg gtg gcg ttg cat ttg   10512
Val Ala Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu
    3490   3495   3500

gcg tgc cag tcg ctg cgt tcg ggt gag tgt gat atg gcg ttg gca ggt   10560
Ala Cys Gln Ser Leu Arg Ser Gly Glu Cys Asp Met Ala Leu Ala Gly
3505   3510   3515   3520

ggt gtg acg gtg atg tcg aca ccc ctg gct ttc ctc gag ttc tct cgt   10608
Gly Val Thr Val Met Ser Thr Pro Leu Ala Phe Leu Glu Phe Ser Arg
                3525   3530   3535

cag cgc ggt ttg gcg cca gat ggt cgg tgc aag tcg ttt gcg gcc gct   10656
Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Lys Ser Phe Ala Ala Ala
            3540   3545   3550

gcg gat ggc acc ggg tgg ggt gag ggt gcc ggc ctg gtg ttg ctg gag   10704
Ala Asp Gly Thr Gly Trp Gly Glu Gly Ala Gly Leu Val Leu Leu Glu
        3555   3560   3565

cgg ttg tcg gat gct cgt cgg aat ggt cac cgg gtg ttg gcc gtg gtt   10752
Arg Leu Ser Asp Ala Arg Arg Asn Gly His Arg Val Leu Ala Val Val
    3570   3575   3580

cgc ggg tct gcg gtg aat cag gat ggt gcg tcg aat ggc ctg act gcg   10800
Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala
3585   3590   3595   3600

244

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ccg aat ggt ccg tcg cag cag cgg gtg att cgg cag gcc ctc gcg aat    10848
Pro Asn Gly Pro Ser Gln Gln Arg Val Ile Arg Gln Ala Leu Ala Asn
            3605             3610             3615

gcg ggg ctg tcg gcg tcc gat gtg gat gtc gtg gag gcg cac ggg acc    10896
Ala Gly Leu Ser Ala Ser Asp Val Asp Val Val Glu Ala His Gly Thr
            3620             3625             3630

ggt acc ggg ctc ggg gat ccg atc gag gcg cag gcg ctg atc gcg aca    10944
Gly Thr Gly Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr
            3635             3640             3645

tat ggg cag gag cgg gat cct gag cgg gcc ctg tgg ctg ggg tcg atc    10992
Tyr Gly Gln Glu Arg Asp Pro Glu Arg Ala Leu Trp Leu Gly Ser Ile
         3650             3655             3660

aag tcc aac atc ggc cac acg cag gcg gcg gcc ggt gtg gcg ggg gtc    11040
Lys Ser Asn Ile Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val
3665             3670             3675             3680

atc aag atg gtg cag gcc atg cgg cac ggg gag ttg cct gcg acg ttg    11088
Ile Lys Met Val Gln Ala Met Arg His Gly Glu Leu Pro Ala Thr Leu
            3685             3690             3695

cac gtg gac aag ccc act cca cag gtg gac tgg tct gcc ggg gcc gtt    11136
His Val Asp Lys Pro Thr Pro Gln Val Asp Trp Ser Ala Gly Ala Val
            3700             3705             3710

cgg ctc ctc acc ggg aac acg ccc tgg ccc gag agc ggc cgt cct cgt    11184
Arg Leu Leu Thr Gly Asn Thr Pro Trp Pro Glu Ser Gly Arg Pro Arg
            3715             3720             3725

cga gcg ggg gtg tcg tcg ttc ggg atc agc ggc acc aac gca cac ctc    11232
Arg Ala Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Leu
         3730             3735             3740

atc ctc gaa caa cca ccg tcg gaa cca gcg gag atc gac caa tcg gat    11280
Ile Leu Glu Gln Pro Pro Ser Glu Pro Ala Glu Ile Asp Gln Ser Asp
3745             3750             3755             3760

cgg cgg gtc act gcg cat cca gcg gtg atc ccg tgg atg ttg tcg gct    11328
Arg Arg Val Thr Ala His Pro Ala Val Ile Pro Trp Met Leu Ser Ala
            3765             3770             3775

agg agt ctc gca gcg ctg cag gcc caa gcg gct gcg ctg cag gcc cgg    11376
Arg Ser Leu Ala Ala Leu Gln Ala Gln Ala Ala Ala Leu Gln Ala Arg
            3780             3785             3790
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ctg gac cgg ggt cct ggc gct tct ccg ctg gat ttg ggg tat tca ctc   11424
Leu Asp Arg Gly Pro Gly Ala Ser Pro Leu Asp Leu Gly Tyr Ser Leu   . ·
        3795   3800   3805

gcg acc act cgt tct gtg ctg gac gaa cgc gcc gtc gtg tgg ggt gcc   11472
Ala Thr Thr Arg Ser Val Leu Asp Glu Arg Ala Val Val Trp Gly Ala
        3810   3815   3820

gat cgg gag gca ctg ctg tcc agg ctg gca gcg ctc gcc gat ggc cgg   11520
Asp Arg Glu Ala Leu Leu Ser Arg Leu Ala Ala Leu Ala Asp Gly Arg
3825   3830   3835   3840

acg gcg ccg ggg gtg ata acg ggc tct gcg aat tcc ggt ggc cgc atc   11568
Thr Ala Pro Gly Val Ile Thr Gly Ser Ala Asn Ser Gly Gly Arg Ile
            3845   3850   3855

gga ttc gtt ttt tcc ggt cag ggc agt cag tgg ctg ggg atg gga aag   11616
Gly Phe Val Phe Ser Gly Gln Gly Ser Gln Trp Leu Gly Met Gly Lys
            3860   3865   3870

gcg ttg tgc gcg gct ttc ccg gcg ttc gcg gac gcc ttc gag gaa gcc   11664
Ala Leu Cys Ala Ala Phe Pro Ala Phe Ala Asp Ala Phe Glu Glu Ala
        3875   3880   3885

tgc gac gcg cta agc gca cac ctg ggc gcg gac gtt cgg ggt gtg ctg   11712
Cys Asp Ala Leu Ser Ala His Leu Gly Ala Asp Val Arg Gly Val Leu
        3890   3895   3900

ttc ggt gct gat gag cag atg ctc gac cgg acg ctg tgg gcg cag tcg   11760
Phe Gly Ala Asp Glu Gln Met Leu Asp Arg Thr Leu Trp Ala Gln Ser
3905   3910   3915   3920

ggg atc ttc gcg gtt caa gtc ggc ctc ctg gga ttg ctg agg tcg tgg   11808
Gly Ile Phe Ala Val Gln Val Gly Leu Leu Gly Leu Leu Arg Ser Trp
            3925   3930   3935

ggc gtg cgg ccg gcc gcg gtg ctg ggg cac tcg gtc ggc gag ttg gct   11856
Gly Val Arg Pro Ala Ala Val Leu Gly His Ser Val Gly Glu Leu Ala
            3940   3945   3950

gcg gcg cac gcg gct ggt gtg ttg tcc ttg ccg gac gct gca cgg ttg   11904
Ala Ala His Ala Ala Gly Val Leu Ser Leu Pro Asp Ala Ala Arg Leu
            3955   3960   3965

gtt gcg gct cgg gcc cac ctg atg cag gca ttg ccc acc ggc ggc gca   11952
Val Ala Ala Arg Ala His Leu Met Gln Ala Leu Pro Thr Gly Gly Ala
        3970   3975   3980

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atg ctc gcg gtc gcc acc agc gag gcg gcg gtc gga ccg ctg ctt tcc     12000
Met Leu Ala Val Ala Thr Ser Glu Ala Ala Val Gly Pro Leu Leu Ser
3985            3990            3995            4000


ggg gtg tgc gat cgg gtc agc atc gct gcg atc aac ggc ccc gag tcg     12048
Gly Val Cys Asp Arg Val Ser Ile Ala Ala Ile Asn Gly Pro Glu Ser
            4005            4010            4015


gta gtg ctc tcc ggc gac cgc gat gtg ctc gtg gag ctc gca ggc gaa     12096
Val Val Leu Ser Gly Asp Arg Asp Val Leu Val Glu Leu Ala Gly Glu
            4020            4025            4030


ttc gat gcc cga ggg ctt agg acc aaa tgg ttg cgg gtc tcc cat gct     12144
Phe Asp Ala Arg Gly Leu Arg Thr Lys Trp Leu Arg Val Ser His Ala
            4035            4040            4045


ttc cac tcg cac cgg atg gaa ccg att ctg gac gag tac gcg gaa acc     12192
Phe His Ser His Arg Met Glu Pro Ile Leu Asp Glu Tyr Ala Glu Thr
            4050            4055            4060


gcc agg tgc gtc gag ttc ggt gaa ccg gtg gtg ccg atc gtc tcc gcc     12240
Ala Arg Cys Val Glu Phe Gly Glu Pro Val Val Pro Ile Val Ser Ala
4065            4070            4075            4080


gcg acc ggt gcg ctg gac acc acc gga ctg atg tgc gcg gcc gac tac     12288
Ala Thr Gly Ala Leu Asp Thr Thr Gly Leu Met Cys Ala Ala Asp Tyr
            4085            4090            4095


tgg acg cgc caa gtg cgt gat cct gtc cgc ttc gga gac ggt gtc cgg     12336
Trp Thr Arg Gln Val Arg Asp Pro Val Arg Phe Gly Asp Gly Val Arg
            4100            4105            4110


gcg ctc gtc ggc caa ggc gtg gac acg atc gtc gag ttc ggc ccg gac     12384
Ala Leu Val Gly Gln Gly Val Asp Thr Ile Val Glu Phe Gly Pro Asp
            4115            4120            4125


ggg gcg ttg tcg gcc ctg gtc gag cag tgc ttg gcc ggg tcc gac cag     12432
Gly Ala Leu Ser Ala Leu Val Glu Gln Cys Leu Ala Gly Ser Asp Gln
            4130            4135            4140


gct ggg agg gtg gcg gcg atc ccg ctg atg cgc agg gac cgc gat gag     12480
Ala Gly Arg Val Ala Ala Ile Pro Leu Met Arg Arg Asp Arg Asp Glu
4145            4150            4155            4160


gtc gag acc gcg gtg gcg gcc ctg gcg cac gtg cac gtc cgc ggt ggt     12528
Val Glu Thr Ala Val Ala Ala Leu Ala His Val His Val Arg Gly Gly
            4165            4170            4175
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247

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gcg gtg gac tgg tcg gct tgc ttc gcc ggc acc ggc gcc cgc acc gtc        12576
Ala Val Asp Trp Ser Ala Cys Phe Ala Gly Thr Gly Ala Arg Thr Val
          4180              4185              4190


gag ttg ccc acc tac gcc ttc caa cgc cag cgg tac tgg ctg gcc ggg        12624
Glu Leu Pro Thr Tyr Ala Phe Gln Arg Gln Arg Tyr Trp Leu Ala Gly
          4195              4200              4205


caa gcg gac ggg cgc ggc ggc gat gtg gtt gcc gac ccg gtc gac gcg        12672
Gln Ala Asp Gly Arg Gly Gly Asp Val Val Ala Asp Pro Val Asp Ala
      4210              4215              4220


cgc ttc tgg gag ttg gtc gag cgc gcc gat ccg gaa ccg ttg gtg gat        12720
Arg Phe Trp Glu Leu Val Glu Arg Ala Asp Pro Glu Pro Leu Val Asp
4225              4230              4235              4240


gaa ctc tgc atc gac cgg gac cag ccc ttc cgg gag gtg ctg ccc gtt        12768
Glu Leu Cys Ile Asp Arg Asp Gln Pro Phe Arg Glu Val Leu Pro Val
              4245              4250              4255


ctg gct tcc tgg cgc gag aaa caa cgc cag gag gcc ctc gcg gat tcc        12816
Leu Ala Ser Trp Arg Glu Lys Gln Arg Gln Glu Ala Leu Ala Asp Ser
          4260              4265              4270


tgg cgc tac cag gtg cgc tgg agg tcc gtc gag gtg ccg tcc gca gcc        12864
Trp Arg Tyr Gln Val Arg Trp Arg Ser Val Glu Val Pro Ser Ala Ala
          4275              4280              4285


gcc ctc cgg ggc gtg tgg ctg gtg gtg ctt cca gct gac gtg ccc cga        12912
Ala Leu Arg Gly Val Trp Leu Val Val Leu Pro Ala Asp Val Pro Arg
          4290              4295              4300


gat caa ccg gcg gtc gtc atc gac gcg ctg atc gcg cgc ggc gcc gag        12960
Asp Gln Pro Ala Val Val Ile Asp Ala Leu Ile Ala Arg Gly Ala Glu
4305              4310              4315              4320


gtc gcg gtc ctg gaa ttg acc gag cag gac ctc caa cgc agt gcg ctt        13008
Val Ala Val Leu Glu Leu Thr Glu Gln Asp Leu Gln Arg Ser Ala Leu
              4325              4330              4335


gtg gac aag gtg cgc gcc gtc att gcg gac cgc acc gag gtg acg ggt        13056
Val Asp Lys Val Arg Ala Val Ile Ala Asp Arg Thr Glu Val Thr Gly
          4340              4345              4350


gtg ttg tct ctg ttg gcg atg gac ggc atg ccc tgc gcg gcg cat ccg        13104
Val Leu Ser Leu Leu Ala Met Asp Gly Met Pro Cys Ala Ala His Pro
          4355              4360              4365
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cac ctg tcc cgt ggt gtc gcc gct acc gtg atc ctg acg cag gtg ttg   13152
His Leu Ser Arg Gly Val Ala Ala Thr Val Ile Leu Thr Gln Val Leu
    4370   4375   4380

ggc gat gcg ggt gtt tcc gcc ccg ctg tgg ctg gcc acg acc ggt ggc   13200
Gly Asp Ala Gly Val Ser Ala Pro Leu Trp Leu Ala Thr Thr Gly Gly
4385   4390   4395   4400

gtc gag gcc ggg acc gag gac ggt ccg gcc gat ccg gac cac ggc ttg   13248
Val Glu Ala Gly Thr Glu Asp Gly Pro Ala Asp Pro Asp His Gly Leu
              4405   4410   4415

atc tgg ggg ctc ggc agg gtc gtc ggc ctt gaa cat ccg cag tgg tgg   13296
Ile Trp Gly Leu Gly Arg Val Val Gly Leu Glu His Pro Gln Trp Trp
          4420   4425   4430

ggt ggc ctg atc gac ctt ccg gag aca ctg gac gag acg tcc cgg aac   13344
Gly Gly Leu Ile Asp Leu Pro Glu Thr Leu Asp Glu Thr Ser Arg Asn
          4435   4440   4445

ggg ttg gtg gcc gca ctc gcc ggg acg gcg gcc gaa gat cag ctc gcc   13392
Gly Leu Val Ala Ala Leu Ala Gly Thr Ala Ala Glu Asp Gln Leu Ala
    4450   4455   4460

gtg cgt tca tcc ggg ttg ttc gtt cgc aga gtg gtg cgc gca gcg cgg   13440
Val Arg Ser Ser Gly Leu Phe Val Arg Arg Val Val Arg Ala Ala Arg
4465   4470   4475   4480

aac ccc cgg tca gag aca tgg cgt agc cgg gga acg gtc ctc atc acg   13488
Asn Pro Arg Ser Glu Thr Trp Arg Ser Arg Gly Thr Val Leu Ile Thr
              4485   4490   4495

ggc gga aca ggc gcg ctc ggt gcc gag gtc gca cga tgg ctg gcc cgg   13536
Gly Gly Thr Gly Ala Leu Gly Ala Glu Val Ala Arg Trp Leu Ala Arg
              4500   4505   4510

cgg gga gct gag cac ctg gtg ttg atc agt cgc cgc ggc ccg gaa gct   13584
Arg Gly Ala Glu His Leu Val Leu Ile Ser Arg Arg Gly Pro Glu Ala
          4515   4520   4525

ccc ggc gca gcg gac cta ggg gcc gag ctg act gaa ctc ggc gtg aaa   13632
Pro Gly Ala Ala Asp Leu Gly Ala Glu Leu Thr Glu Leu Gly Val Lys
    4530   4535   4540

gtc aca gtc ttg gcc tgc gat gtg acg gac cgc gac gag ctg gcg gcg   13680
Val Thr Val Leu Ala Cys Asp Val Thr Asp Arg Asp Glu Leu Ala Ala
4545   4550   4555   4560

gtg ctg gcg gcc gtt ccc acg gag tat ccg ctg tcg gcg gtc gtg cac   13728
Val Leu Ala Ala Val Pro Thr Glu Tyr Pro Leu Ser Ala Val Val His
            4565   4570   4575

acc gcc ggc gtc ggg acg cct gcg aac ctg gcc gag acg acc ttg gcg   13776
Thr Ala Gly Val Gly Thr Pro Ala Asn Leu Ala Glu Thr Thr Leu Ala
            4580   4585   4590

cag ttc gcc gac gtg ttg tcg gcc aag gtc gtc ggc gcg gcg aac ctg   13824
Gln Phe Ala Asp Val Leu Ser Ala Lys Val Val Gly Ala Ala Asn Leu
            4595   4600   4605

gac cgg ctg ctt ggc ggg caa ccg ttg gac gcc ttc gtg ctg ttc tcc   13872
Asp Arg Leu Leu Gly Gly Gln Pro Leu Asp Ala Phe Val Leu Phe Ser
        4610   4615   4620

tcg atc tcg gga gtt tgg gga gcc ggc ggc caa gga gcc tat tcg gcc   13920
Ser Ile Ser Gly Val Trp Gly Ala Gly Gly Gln Gly Ala Tyr Ser Ala
4625   4630   4635   4640

gcc aat gcg tat ctc gat gcc ctt gcc gag cgc cga cgg gct tgc ggg   13968
Ala Asn Ala Tyr Leu Asp Ala Leu Ala Glu Arg Arg Arg Ala Cys Gly
            4645   4650   4655

cgg ccg gcg acg tgc atc gcc tgg ggt ccg tgg gcg ggt gcg ggc atg   14016
Arg Pro Ala Thr Cys Ile Ala Trp Gly Pro Trp Ala Gly Ala Gly Met
            4660   4665   4670

gcc gtt cag gaa ggt aac gag gcg cat ctc cgc cga agg ggc ctg gta   14064
Ala Val Gln Glu Gly Asn Glu Ala His Leu Arg Arg Arg Gly Leu Val
            4675   4680   4685

ccg atg gaa ccg cag tcg gcc ctc ttc gcg ctg caa cag gcc ctg tcc   14112
Pro Met Glu Pro Gln Ser Ala Leu Phe Ala Leu Gln Gln Ala Leu Ser
            4690   4695   4700

caa cga gaa acc gcc atc acc gtc gca gat gtg gac tgg gag cga ttc   14160
Gln Arg Glu Thr Ala Ile Thr Val Ala Asp Val Asp Trp Glu Arg Phe
4705   4710   4715   4720

gcc gcc tct ttc acc gcg gcc cgc ccg cga cca ctg ttg gaa gag atc   14208
Ala Ala Ser Phe Thr Ala Ala Arg Pro Arg Pro Leu Leu Glu Glu Ile
            4725   4730   4735

gtg gat cta cgg ccc gac acc gag acc gag gag aag cac ggt gcc ggc   14256
Val Asp Leu Arg Pro Asp Thr Glu Thr Glu Glu Lys His Gly Ala Gly
            4740   4745   4750

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gag ctg ggg cag cag ctg gcc gca ctg ccg ccc gct gag cgc gga cac    14304
Glu Leu Gly Gln Gln Leu Ala Ala Leu Pro Pro Ala Glu Arg Gly His
        4755            4760            4765


ctg ctg ctg gag gtg gtg ctg gcg gaa acc gcc agc acc ctg ggg cac    14352
Leu Leu Leu Glu Val Val Leu Ala Glu Thr Ala Ser Thr Leu Gly His
        4770            4775            4780


gat tcg gcg gag gct gtg caa ccc gat cgg acc ttc gcc gaa ctg ggc    14400
Asp Ser Ala Glu Ala Val Gln Pro Asp Arg Thr Phe Ala Glu Leu Gly
4785            4790            4795            4800


ttc gat tcg ctg acc gcg gta gag ctg cgc aac agg ttg aac gcg gtg    14448
Phe Asp Ser Leu Thr Ala Val Glu Leu Arg Asn Arg Leu Asn Ala Val
         4805            4810            4815


acc ggg ctt cgc ctg ccg ccg acg ctg gtt ttc gac cac ccg acg ccg    14496
Thr Gly Leu Arg Leu Pro Pro Thr Leu Val Phe Asp His Pro Thr Pro
            4820            4825            4830


ctg gcg ttg tcc gaa cag ttg gtt ccg gcc ctg gtc gcg gag ccg gac    14544
Leu Ala Leu Ser Glu Gln Leu Val Pro Ala Leu Val Ala Glu Pro Asp
        4835            4840            4845


aac ggc atc gaa tcg ctg ctc gcc gag ctc gac agg ctg gat acc acg    14592
Asn Gly Ile Glu Ser Leu Leu Ala Glu Leu Asp Arg Leu Asp Thr Thr
        4850            4855            4860


ttg gcg caa ggg cct tcg atc cca ctg gaa gac cag gcc aag gtg gcg    14640
Leu Ala Gln Gly Pro Ser Ile Pro Leu Glu Asp Gln Ala Lys Val Ala
4865            4870            4875            4880


gag cgc ttg cac gca ctc ctc gcc aag tgg gac ggg gcg cgt gac ggc    14688
Glu Arg Leu His Ala Leu Leu Ala Lys Trp Asp Gly Ala Arg Asp Gly
            4885            4890            4895


acg gcc aga gcg acg tca ccc caa tcg ctg acg gcg gcc acg gac gac    14736
Thr Ala Arg Ala Thr Ser Pro Gln Ser Leu Thr Ala Ala Thr Asp Asp
            4900            4905            4910


gaa atc ttc gac ctc atc gac cgg aag ttc cgg cgc tga    14775
Glu Ile Phe Asp Leu Ile Asp Arg Lys Phe Arg Arg
        4915            4920
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<210> 48
<211> 4924
<212> PRT
```

<213> Saccharopolyspora spinosa

<400> 48
Met Ala Asn Glu Glu Lys Leu Phe Gly Tyr Leu Lys Lys Val Thr Ala
1   5   10   15

Asp Leu His Gln Thr Arg Gln Arg Leu Leu Ala Ala Glu Ser Arg Ser
            20   25   30

Gln Glu Pro Ile Ala Ile Val Ser Ala Ser Cys Arg Leu Pro Gly Gly
        35   40   45

Val Asp Ser Pro Glu Ala Leu Trp Gln Leu Val Arg Thr Gly Thr Asp
    50   55   60

Ala Ile Ser Glu Phe Pro Ala Asp Arg Gly Trp Asp Leu Gly Arg Leu
65   70   75   80

Tyr Asp Pro Asp Pro Asn His Gln Gly Thr Ser Tyr Thr Arg Ala Gly
            85   90   95

Gly Phe Leu Ala Gly Ala Gly Asp Phe Asp Pro Ala Met Phe Gly Ile
            100   105   110

Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg Leu Leu Leu
        115   120   125

Glu Leu Ser Trp Glu Ala Leu Glu Arg Ala Gly Ile Asp Pro Thr Ser
    130   135   140

Leu Arg Gly Ser Lys Thr Gly Val Phe Gly Gly Val Thr Pro Gln Glu
145   150   155   160

Tyr Gly Pro Ser Leu Gln Glu Met Ser Arg Asn Ala Gly Gly Phe Gly
            165   170   175

Leu Thr Gly Arg Met Val Ser Val Ala Ser Gly Arg Val Ala Tyr Ser
            180   185   190

Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser
        195   200   205

Ser Leu Val Ala Leu His Leu Ala Cys Gln Ser Leu Arg Ser Gly Glu
    210   215   220

Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met Ala Thr Pro Ala
225   230   235   240

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Thr Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala Pro Asp Gly Arg
             245                 250                 255

Cys Lys Ser Phe Ala Ala Ala Ala Asp Gly Thr Gly Trp Gly Glu Gly
             260                 265                 270

Ala Gly Leu Val Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly
             275                 280                 285

His Glu Val Leu Ala Val Val Arg Gly Ser Ala Val Asn Gln Asp Gly
         290                 295                 300

Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser Gln Gln Arg Val
305                 310                 315                 320

Ile Thr Gln Ala Leu Ala Ser Ala Gly Leu Ser Val Ser Asp Val Asp
                 325                 330                 335

Ala Val Glu Ala His Gly Thr Gly Thr Thr Leu Gly Asp Pro Ile Glu
             340                 345                 350

Ala Gln Ala Leu Ile Ala Thr Tyr Gly Gln Gly Arg Glu Lys Asp Arg
             355                 360                 365

Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile Gly His Thr Gln Ala
     370                 375                 380

Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Leu Ala Met Arg His
385                 390                 395                 400

Gly Gln Leu Pro Ala Thr Leu His Val Asp Glu Pro Thr Ser Ala Val
                 405                 410                 415

Asp Trp Ser Ala Gly Ser Val Arg Leu Leu Thr Glu Asn Thr Pro Trp
             420                 425                 430

Pro Asp Ser Gly Arg Pro Cys Arg Val Gly Val Ser Ser Phe Gly Ile
             435                 440                 445

Ser Gly Thr Asn Ala His Val Ile Leu Glu Gln Ser Pro Val Glu Gln
     450                 455                 460

Gly Glu Pro Ala Gly Pro Val Glu Gly Glu Arg Glu Pro Asp Val Ala
465                 470                 475                 480

Val Pro Val Val Pro Trp Val Leu Ser Gly Lys Thr Pro Glu Ala Ala
                 485                 490                 495
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Arg Ala Gln Ala Glu Arg Val His Ser His Ile Glu Asp Arg Pro Gly
        500              505              510

Leu Ser Pro Val Asp Val Ala Tyr Ser Leu Gly Met Thr Arg Ala Ala
        515              520              525

Leu Asp Glu Arg Ala Val Val Leu Gly Ser Asp Arg Ala Ala Leu Leu
        530              535              540

Thr Gly Leu Arg Ala Phe Ala Asp Gly Cys Asp Ala Pro Glu Val Val
545              550              555              560

Ser Gly Ser Val Gly Leu Gly Gly Arg Val Gly Phe Val Phe Ser Gly
            565              570              575

Gln Gly Gly Gln Trp Pro Gly Met Gly Arg Gly Leu Tyr Ser Val Phe
        580              585              590

Pro Val Phe Ala Asp Ala Phe Asp Glu Ala Cys Ala Glu Leu Asp Ala
        595              600              605

His Leu Gly Gln Glu Leu Arg Val Arg Asp Val Val Phe Gly Ser Gln
        610              615              620

Ala Trp Leu Leu Asp Arg Thr Val Trp Ala Gln Ser Gly Leu Phe Ala
625              630              635              640

Leu Gln Ile Gly Leu Leu Arg Leu Leu Gly Ser Trp Gly Val Arg Pro
            645              650              655

Asp Val Val Leu Gly His Ser Val Gly Glu Leu Ala Ala Val His Ala
        660              665              670

Ala Gly Val Leu Ser Leu Ser Glu Ala Ala Arg Leu Val Ala Gly Arg
        675              680              685

Ala Arg Leu Met Gln Ala Leu Pro Ser Gly Gly Ala Met Leu Ala Val
        690              695              700

Ala Thr Gly Glu Phe Gln Val Asp Pro Leu Leu Asp Gly Val Arg Asp
705              710              715              720

Arg Ile Gly Ile Ala Ala Val Asn Gly Pro Glu Ser Val Val Leu Ser
            725              730              735

Gly Asp Arg Glu Leu Leu Thr Glu Ile Ala Asp Arg Leu His Asp Gln
            740              745              750
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Gly Cys Arg Thr Arg Trp Leu Arg Val Ser His Ala Phe His Ser Pro
        755             760             765

His Met Glu Pro Met Leu Glu Glu Phe Ala Gln Ile Ser Arg Gly Arg
        770             775             780

Glu Tyr His Ala Pro Glu Leu Pro Ile Ile Ser Thr Leu Ile Gly Glu
785             790             795             800

Leu Asp Gly Gly Arg Val Met Gly Thr Pro Glu Tyr Trp Val Arg Gln
                805             810             815

Val Arg Glu Pro Val Arg Phe Ala Glu Gly Val Gln Ala Leu Val Gly
        820             825             830

Gln Gly Val Gly Thr Ile Val Glu Leu Gly Pro Asp Gly Ala Leu Ser
        835             840             845

Thr Leu Val Glu Glu Cys Val Ala Glu Ser Gly Arg Val Ala Gly Ile
    850             855             860

Pro Leu Met Arg Lys Asp Arg Asp Glu Ala Arg Thr Val Leu Ala Ala
865             870             875             880

Leu Ala Gln Ile His Thr Arg Gly Gly Glu Val Asp Trp Arg Ser Phe
            885             890             895

Phe Ala Gly Thr Gly Ala Lys Gln Val Asp Leu Pro Thr Tyr Ala Phe
        900             905             910

Gln Arg Gln Arg Tyr Trp Leu Ala Ser Thr Gly Arg Ala Gly Asp Val
        915             920             925

Thr Ala Ala Gly Leu Ala Glu Ala Asp His Pro Leu Leu Gly Ala Val
    930             935             940

Val Ala Leu Ala Asp Gly Glu Gly Val Val Leu Thr Gly Arg Leu Thr
945             950             955             960

Ala Gly Ser His Pro Trp Leu Ser Asp His Arg Val Leu Gly Glu Ile
            965             970             975

Val Val Pro Gly Thr Ala Ile Val Glu Leu Val Trp His Val Gly Glu
        980             985             990

Arg Leu Gly Cys Gly Arg Val Glu Glu Leu Ala Leu Glu Ala Pro Leu
        995             1000            1005
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255

Ile Leu Pro Asp His Gly Ala Val Gln Val Gln Val Leu Val Gly Pro
    1010   1015   1020

Pro Gly Glu Ser Gly Ala Arg Ser Val Ala Leu Tyr Ser Cys Pro Gly
025   1030   1035   1040

Glu Ala Ile Glu Pro Glu Trp Lys Lys His Ala Thr Gly Val Leu Leu
            1045   1050   1055

Pro Pro Val Ala Ala Glu Asn His Glu Leu Thr Ala Trp Pro Pro Glu
            1060   1065   1070

Asn Ala Thr Glu Ile Asp Ala Asp Gly Val Tyr Ala Phe Leu Glu Gly
            1075   1080   1085

His Gly Phe Ala Tyr Gly Pro Ala Phe Arg Cys Leu Arg Gly Ala Trp
            1090   1095   1100

Arg Arg Gly Gly Glu Val Phe Ala Glu Val Ala Leu Pro Asp Asp Met
105   1110   1115   1120

Gln Ala Gly Val Asp Arg Phe Gly Val His Pro Ala Leu Leu Asp Ala
            1125   1130   1135

Val Leu His Ala Ala Ala Ala Glu Thr Ser Val Val Gln Ser Glu Ala
            1140   1145   1150

Arg Val Pro Phe Ser Trp Arg Gly Val Glu Leu Arg Ala Thr Glu Ser
            1155   1160   1165

Ala Val Val Arg Ala Arg Leu Ser Leu Thr Ser Asp Asp Glu Leu Ser
    1170   1175   1180

Leu Val Ala Val Asp Pro Ala Gly Arg Phe Val Ala Thr Val Asp Ser
185   1190   1195   1200

Leu Val Thr Arg Pro Ile Ser Arg Gln Gln Val Arg Ser Gly Ala Ile
            1205   1210   1215

Gly Asp Cys Leu Phe Glu Val Glu Trp His Arg Lys Ala Leu Leu Gly
            1220   1225   1230

Thr Thr Ala Gly Asp Asp Leu Ala Ile Val Gly Asp Gly Pro Ser Trp
    1235   1240   1245

Pro Glu Ser Val Arg Ala Thr Ala Arg Phe Ala Thr Leu Asp Glu Phe
    1250   1255   1260

256

Arg Ala Ala Val Asp Ser Asp Val Pro Ala Pro Gly Ser Val Leu Val
265   1270   1275   1280

Ala Ala Met Ser Ala Glu Glu Val Glu Gly Gly Ser Leu Pro Ser Arg
        1285   1290   1295

Ala Gln Glu Ser Thr Ser Asp Leu Leu Ala Leu Val Gln Ser Trp Leu
     1300   1305   1310

Ala Asp Glu Arg Phe Ala Glu Ser Gln Leu Val Val Val Thr Arg Ala
     1315   1320   1325

Ala Val Ser Ala Asp Ser Asp Ser Asp Val Ala Asp Leu Val Gly Ala
     1330   1335   1340

Ser Ser Trp Gly Leu Leu Ser Ser Ala Gln Ser Glu Asn Pro Gly Arg
345   1350   1355   1360

Phe Val Leu Val Asp Val Asp Gly Thr Pro Glu Ser Trp Gln Ala Leu
        1365   1370   1375

Pro Ala Ala Val Arg Ala Gly Glu Pro Gln Leu Ala Leu Arg Arg Gly
        1380   1385   1390

Val Ala Leu Val Pro Arg Leu Ala Arg Leu Thr Val Arg Glu Glu Gly
     1395   1400   1405

Ser Ser Pro Gln Leu Asp Thr Asp Gly Thr Val Leu Ile Thr Gly Gly
     1410   1415   1420

Thr Gly Ala Leu Gly Gly Val Val Ala Arg His Leu Val Glu Glu His
425   1430   1435   1440

Gly Ile Arg Arg Leu Val Leu Ala Gly Arg Arg Gly Trp Asn Ala Pro
        1445   1450   1455

Gly Val His Glu Leu Val Asp Glu Leu Ala Arg Ala Gly Ala Val Val
        1460   1465   1470

Glu Val Val Ala Cys Asp Val Ala Asp Arg Thr Asp Leu Glu His Val
        1475   1480   1485

Leu Ala Ala Ile Pro Val Asp Trp Pro Leu Arg Gly Ile Val His Thr
     1490   1495   1500

Ala Gly Val Leu Ala Asp Gly Val Ile Gly Ser Leu Ser Ala Ala Asp
505   1510   1515   1520

257

Val Gly Thr Val Phe Ala Pro Lys Val Thr Gly Ala Trp His Leu His
                1525   1530   1535

Glu Leu Thr Arg Asp Leu Asp Leu Ser Phe Phe Val Leu Phe Ser Ser
        1540   1545   1550

Phe Ser Gly Ile Ala Gly Ala Ala Gly Gln Ala Asn Tyr Ala Ala Ala
        1555   1560   1565

Asn Thr Phe Leu Asp Ala Leu Ala Arg Tyr Arg Arg Ala Arg Gly Leu
        1570   1575   1580

Pro Gly Leu Ser Leu Ala Trp Gly Leu Trp Ala Gln Pro Ser Gly Met
 585   1590   1595   1600

Thr Ser Gly Leu Asp Ala Ala Ser Val Glu Arg Leu Ala Arg Thr Gly
                1605   1610   1615

Ile Ala Glu Leu Ser Thr Glu Asp Gly Leu Arg Leu Phe Asp Ala Ala
            1620   1625   1630

Phe Ala Lys Asp Arg Ala Cys Val Val Ala Ala Arg Leu Asp Arg Ala
            1635   1640   1645

Leu Leu Val Gly Asn Gly Arg Ser His Ala Ile Pro Ala Leu Leu Ser
        1650   1655   1660

Ala Leu Val Pro Val Arg Gly Gly Val Ala Arg Lys Thr Ala Asn Ser
 665   1670   1675   1680

Gln Ala Ala Asp Glu Asp Ala Leu Leu Gly Leu Val Arg Glu His Val
                1685   1690   1695

Ser Ala Val Leu Gly Tyr Ser Gly Ala Val Glu Val Gly Gly Asp Arg
            1700   1705   1710

Ala Phe Arg Asp Leu Gly Phe Asp Ser Leu Ser Gly Val Glu Leu Arg
        1715   1720   1725

Asn Arg Leu Ala Gly Val Leu Gly Val Arg Leu Pro Ala Thr Ala Val
        1730   1735   1740

Phe Asp Tyr Pro Thr Pro Arg Ala Leu Ala Arg Phe Leu His Gln Glu
 745   1750   1755   1760

Leu Ala Gly Glu Val Ala Ser Thr Ser Thr Pro Val Thr Arg Ala Ala
            1765   1770   1775

258

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Ser Ala Glu Glu Asp Leu Val Ala Ile Val Gly Met Gly Cys Arg Phe
        1780            1785            1790

Pro Gly Gly Val Ser Ser Pro Glu Glu Leu Trp Arg Leu Val Ala Gly
        1795            1800            1805

Gly Val Asp Ala Val Ala Gly Phe Pro Asp Asp Arg Gly Trp Asp Leu
    1810            1815            1820

Ala Ala Leu Tyr Asp Pro Asp Pro Asp Arg Leu Gly Thr Ser Tyr Val
825             1830            1835            1840

Cys Glu Gly Gly Phe Leu Arg Asp Ala Ala Glu Phe Asp Ala Asp Met
            1845            1850            1855

Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg
        1860            1865            1870

Leu Leu Leu Glu Val Ala Trp Glu Thr Leu Glu Arg Ala Gly Ile Asp
        1875            1880            1885

Pro Phe Ser Leu His Gly Ser Arg Thr Gly Val Phe Ala Gly Leu Met
    1890            1895            1900

Tyr His Asp Tyr Gly Ala Arg Phe Ile Thr Arg Ala Pro Glu Gly Phe
905             1910            1915            1920

Glu Gly His Leu Gly Thr Gly Asn Ala Gly Ser Val Leu Ser Gly Arg
            1925            1930            1935

Val Ala Tyr Ser Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr
        1940            1945            1950

Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala Gly Gln Ala Leu
        1955            1960            1965

Arg Ala Gly Glu Cys Glu Phe Ala Leu Ala Gly Gly Val Thr Val Met
    1970            1975            1980

Ser Thr Pro Thr Thr Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala
985             1990            1995            2000

Pro Asp Gly Arg Cys Lys Ser Phe Ala Ala Ala Ala Asp Gly Thr Gly
            2005            2010            2015

Trp Gly Glu Gly Ala Gly Leu Val Leu Leu Glu Arg Leu Ser Asp Ala
        2020            2025            2030
```

Arg Arg Asn Gly His Glu Val Leu Ala Val Val Arg Gly Ser Ala Val
    2035   2040   2045

Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser
    2050   2055   2060

Gln Gln Arg Val Ile Thr Gln Ala Leu Thr Ser Ala Gly Leu Ser Val
065   2070   2075   2080

Ser Asp Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly
            2085   2090   2095

Asp Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr Tyr Gly Arg Asp Arg
        2100   2105   2110

Asp Pro Gly Arg Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile Gly
        2115   2120   2125

His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Met
    2130   2135   2140

Ala Met Arg Gln Gly Glu Leu Pro Arg Thr Leu His Val Asp Glu Pro
145   2150   2155   2160

Ser Ala Gln Val Asp Trp Ser Ala Gly Thr Val Gln Leu Leu Thr Glu
            2165   2170   2175

Asn Thr Pro Trp Pro Asp Ser Gly Arg Leu Arg Arg Ala Gly Val Ser
        2180   2185   2190

Ser Phe Gly Ile Ser Gly Thr Asn Ala His Leu Ile Leu Glu Gln Pro
        2195   2200   2205

Pro Arg Glu Ser Gln Arg Ser Thr Glu Pro Asp Ser Gly Ser Val Arg
    2210   2215   2220

Asp Phe Pro Val Val Pro Trp Met Val Ser Gly Lys Thr Pro Glu Ala
225   2230   2235   2240

Leu Ser Ala Gln Ala Asp Ala Leu Met Ser Tyr Leu Ser Asn Arg Val
            2245   2250   2255

Asp Ala Ser Pro Arg Asp Ile Gly Tyr Ser Leu Ala Val Thr Arg Pro
        2260   2265   2270

Ala Leu Asp His Arg Ala Val Val Leu Gly Ala Asp Arg Ala Ala Leu
        2275   2280   2285

260

Leu Pro Gly Leu Lys Ala Leu Ala Val Ser Asn Asp Ala Ala Glu Val
    2290   2295   2300

Ile Thr Gly Thr Arg Ala Ala Gly Pro Val Gly Phe Val Phe Ser Gly
305   2310   2315   2320

Gln Gly Gly Gln Trp Pro Gly Met Gly Ser Gly Leu His Ser Ala Phe
             2325   2330   2335

Pro Val Phe Ala Asp Ala Phe Asp Glu Ala Cys Cys Glu Leu Asp Ala
         2340   2345   2350

His Leu Gly Gln Met Ala Arg Leu Arg Asp Val Leu Ser Gly Ser Asp
    2355   2360   2365

Thr Gln Leu Leu Asp Gln Thr Leu Trp Ala Gln Pro Gly Leu Phe Ala
    2370   2375   2380

Leu Gln Val Gly Leu Trp Glu Leu Leu Gly Ser Trp Gly Val Arg Pro
385   2390   2395   2400

Ala Val Val Leu Gly His Ser Val Gly Glu Leu Ala Ala Ala Phe Ala
             2405   2410   2415

Ala Gly Val Leu Ser Leu Arg Asp Ala Ala Arg Leu Val Ala Gly Arg
         2420   2425   2430

Ala Arg Leu Met Gln Ala Leu Pro Thr Gly Gly Ala Met Leu Ala Ala
    2435   2440   2445

Ala Ala Gly Glu Glu Gln Leu Arg Pro Leu Leu Ala Asp Cys Gly Asp
    2450   2455   2460

Arg Val Gly Ile Ala Ala Val Asn Ala Pro Gly Ser Val Val Leu Ser
465   2470   2475   2480

Gly Asp Arg Asp Val Leu Asp Asp Ile Ala Gly Arg Leu Asp Gly Gln
             2485   2490   2495

Gly Ile Arg Ser Arg Trp Leu Arg Val Ser His Ala Phe His Ser His
         2500   2505   2510

Arg Met Asp Pro Met Leu Ala Glu Phe Thr Glu Ile Ala Arg Ser Val
    2515   2520   2525

Asp Tyr Arg Ser Ser Gly Leu Pro Ile Val Ser Thr Leu Thr Gly Glu
    2530   2535   2540

Leu Asp Glu Val Gly Met Pro Ala Thr Pro Glu Tyr Trp Val Arg Gln
545   2550   2555   2560

Val Arg Glu Pro Val Arg Phe Ala Asp Gly Val Ala Ala Leu Ala Ala
          2565   2570   2575

His Gly Val Ser Thr Val Val Glu Val Gly Pro Asp Gly Val Leu Ser
          2580   2585   2590

Ala Leu Val Gln Glu Cys Ala Ala Gly Ser Asp Gln Gly Gly Arg Val
     2595   2600   2605

Ala Ala Val Pro Leu Met Arg Ser Asn Arg Asp Glu Ala His Thr Val
     2610   2615   2620

Thr Thr Ala Leu Ala Gln Ile His Val Arg Gly Ala Glu Val Asp Trp
625   2630   2635   2640

Arg Ser Phe Phe Ala Gly Thr Gly Ala Lys Gln Val Glu Leu Pro Thr
          2645   2650   2655

Tyr Ala Phe Gln Arg Gln Arg Tyr Trp Leu Asp Ser Pro Ser Glu Pro
          2660   2665   2670

Val Gly Gln Ser Ala Asp Pro Ala Arg Gln Ser Gly Phe Trp Glu Leu
     2675   2680   2685

Val Glu Gln Glu Asp Val Ser Ala Leu Ser Ala Ala Leu His Ile Thr
     2690   2695   2700

Gly Asp His Asp Val Gln Ala Ser Leu Glu Ser Val Val Pro Val Leu
705   2710   2715   2720

Ser Ser Trp His Arg Arg Ile Arg Asn Glu Ser Leu Val His Gln Trp
          2725   2730   2735

Arg Tyr Arg Ile Ser Trp His Glu Arg Ala Asp Leu Pro Asp Pro Ser
          2740   2745   2750

Leu Ser Gly Thr Trp Leu Val Val Val Pro Glu Gly Trp Ser Ala Ser
          2755   2760   2765

Arg Gln Val Leu Arg Phe Asn Glu Met Phe Glu Glu Arg Gly Cys Pro
     2770   2775   2780

Ala Val Leu Phe Glu Leu Ala Gly His Asp Glu Glu Ala Leu Ala Gln
785   2790   2795   2800

262

Arg Phe Arg Ser Leu Pro Val Ala Ser Gly Gly Ile Ser Gly Val Leu
        2805   2810   2815

Ser Leu Leu Ala Leu Asp Glu Ser Pro Ser Ser Pro Asn Ala Ala Leu
        2820   2825   2830

Pro Asn Gly Ala Leu Asn Ser Leu Val Leu Leu Arg Ala Leu Arg Ala
        2835   2840   2845

Ala Asp Val Ser Ala Pro Leu Trp Leu Ala Thr Cys Gly Gly Val Ala
    2850   2855   2860

Val Gly Asp Val Pro Val Asn Pro Gly Gln Ala Leu Val Trp Gly Leu
865   2870   2875   2880

Gly Arg Val Val Gly Leu Glu His Pro Ala Trp Trp Gly Gly Leu Val
        2885   2890   2895

Asp Val Pro Cys Leu Leu Asp Glu Asp Ala Arg Glu Arg Leu Ser Val
        2900   2905   2910

Val Leu Ala Gly Leu Gly Glu Asp Glu Ile Ala Val Arg Pro Gly Gly
        2915   2920   2925

Val Phe Val Arg Arg Leu Glu Arg Ala Gly Ala Ala Ser Gly Ala Gly
    2930   2935   2940

Ser Val Trp Arg Pro Arg Gly Thr Val Leu Val Thr Gly Gly Thr Gly
945   2950   2955   2960

Gly Leu Gly Ala His Val Ala Arg Trp Leu Ala Gly Ala Gly Ala Glu
        2965   2970   2975

His Val Val Leu Thr Ser Arg Arg Gly Ala Ala Ala Pro Gly Ala Gly
        2980   2985   2990

Asp Leu Arg Ala Glu Leu Glu Ala Leu Gly Ala Arg Val Ser Ile Thr
        2995   3000   3005

Ala Cys Asp Val Ala Asp Arg Asp Ala Leu Ala Glu Val Leu Ala Thr
    3010   3015   3020

Ile Pro Asp Asp Cys Pro Leu Thr Ala Val Met His Ala Ala Gly Val
025   3030   3035   3040

Val Glu Val Gly Asp Val Ala Ser Met Cys Leu Thr Asp Phe Val Gly
        3045   3050   3055

263

Val Leu Ser Ala Lys Ala Gly Gly Ala Ala Asn Leu Asp Glu Leu Leu
        3060   3065   3070

Ala Asp Val Glu Leu Asp Ala Phe Val Leu Phe Ser Ser Val Ser Gly
        3075   3080   3085

Val Trp Gly Ala Gly Gly Gln Gly Ala Tyr Ala Ala Ala Asn Ala Tyr
    3090   3095   3100

Leu Asp Ala Leu Ala Gln Gln Arg Arg Ala Arg Gly Leu Val Gly Thr
105   3110   3115   3120

Ala Val Ala Trp Gly Pro Trp Ala Gly Asp Gly Met Ala Ala Gly Glu
            3125   3130   3135

Gly Gly Ala Gln Leu Arg Arg Ala Gly Leu Val Pro Met Ala Ala Asp
        3140   3145   3150

Arg Ala Leu Leu Ala Leu Gln Gly Ala Leu Asp Arg Asp Glu Thr Ser
        3155   3160   3165

Leu Val Val Ala Asp Met Ala Trp Glu Arg Phe Ala Pro Val Phe Ala
    3170   3175   3180

Met Ser Arg Arg Arg Pro Leu Leu Asp Glu Leu Pro Glu Ala Gln Gln
185   3190   3195   3200

Ala Leu Ala Asp Ala Glu Asn Thr Thr Asp Ala Ala Asp Ser Ala Val
            3205   3210   3215

Pro Leu Pro Arg Leu Ala Gly Met Ala Ala Ala Glu Arg Arg Arg Ala
        3220   3225   3230

Met Leu Asp Leu Val Leu Ala Glu Ala Ser Ile Val Leu Gly His Asn
        3235   3240   3245

Gly Ser Asp Pro Val Gly Pro Asp Arg Ala Phe Gln Glu Leu Gly Phe
    3250   3255   3260

Asp Ser Leu Met Ala Val Glu Leu Arg Asn Arg Leu Gly Glu Ala Thr
265   3270   3275   3280

Gly Leu Ser Leu Pro Ala Thr Leu Ile Phe Asp Tyr Pro Ser Pro Ser
        3285   3290   3295

Ala Leu Ala Glu Gln Leu Val Gly Glu Leu Val Gly Ala Gln Pro Ala
        3300   3305   3310

264

Thr Thr Val Val Ala Gly Ala Asp Pro Val Asp Asp Pro Val Val Val
    3315   3320   3325

Val Ala Met Gly Cys Arg Tyr Pro Gly Asp Val Cys. Ser Pro Glu Glu
    3330   3335   3340

Leu Trp Gln Leu Val Ser Ala Gly Arg Asp Ala Val Ser Thr Phe Pro
345   3350   3355   3360

Val Asp Arg Gly Trp Asp Cys Asn Thr Leu Phe Asp Pro Asp Pro Asp
                3365   3370   3375

Arg Ala Gly Ser Thr Tyr Val Arg Glu Gly Ala Phe Leu Thr Gly Ala
                3380   3385   3390

Asp Arg Phe Asp Ala Gly Phe Phe Gly Ile Ser Pro Arg Glu Ala Arg
        3395   3400   3405

Ala Met Asp Pro Gln Gln Arg Leu Leu Leu Glu Val Ala Trp Glu Val
    3410   3415   3420

Phe Glu Arg Ala Gly Ile Ala Pro Leu Ser Leu Arg Gly Ser Arg Thr
425   3430   3435   3440

Gly Val Phe Ala Gly Thr Asn Gly Gln Asp His Gly Ala Lys Val Ala
            3445   3450   3455

Ala Ala Pro Glu Ala Ala Gly His Leu Leu Thr Gly Asn Ala Ala Ser
        3460   3465   3470

Val Leu Ala Gly Arg Leu Ser Tyr Thr Phe Gly Leu Glu Gly Pro Ala
        3475   3480   3485

Val Ala Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu
    3490   3495   3500

Ala Cys Gln Ser Leu Arg Ser Gly Glu Cys Asp Met Ala Leu Ala Gly
505   3510   3515   3520

Gly Val Thr Val Met Ser Thr Pro Leu Ala Phe Leu Glu Phe Ser Arg
            3525   3530   3535

Gln Arg Gly Leu Ala Pro Asp Gly Arg Cys Lys Ser Phe Ala Ala Ala
        3540   3545   3550

Ala Asp Gly Thr Gly Trp Gly Glu Gly Ala Gly Leu Val Leu Leu Glu
        3555   3560   3565

265

Arg Leu Ser Asp Ala Arg Arg Asn Gly His Arg Val Leu Ala Val Val
    3570   3575   3580

Arg Gly Ser Ala Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala
585   3590   3595   3600

Pro Asn Gly Pro Ser Gln Gln Arg Val Ile Arg Gln Ala Leu Ala Asn
            3605   3610   3615

Ala Gly Leu Ser Ala Ser Asp Val Asp Val Val Glu Ala His Gly Thr
            3620   3625   3630

Gly Thr Gly Leu Gly Asp Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr
            3635   3640   3645

Tyr Gly Gln Glu Arg Asp Pro Glu Arg Ala Leu Trp Leu Gly Ser Ile
    3650   3655   3660

Lys Ser Asn Ile Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val
665   3670   3675   3680

Ile Lys Met Val Gln Ala Met Arg His Gly Glu Leu Pro Ala Thr Leu
            3685   3690   3695

His Val Asp Lys Pro Thr Pro Gln Val Asp Trp Ser Ala Gly Ala Val
            3700   3705   3710

Arg Leu Leu Thr Gly Asn Thr Pro Trp Pro Glu Ser Gly Arg Pro Arg
    3715   3720   3725

Arg Ala Gly Val Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Leu
    3730   3735   3740

Ile Leu Glu Gln Pro Pro Ser Glu Pro Ala Glu Ile Asp Gln Ser Asp
745   3750   3755   3760

Arg Arg Val Thr Ala His Pro Ala Val Ile Pro Trp Met Leu Ser Ala
            3765   3770   3775

Arg Ser Leu Ala Ala Leu Gln Ala Gln Ala Ala Ala Leu Gln Ala Arg
    3780   3785   3790

Leu Asp Arg Gly Pro Gly Ala Ser Pro Leu Asp Leu Gly Tyr Ser Leu
    3795   3800   3805

Ala Thr Thr Arg Ser Val Leu Asp Glu Arg Ala Val Val Trp Gly Ala
    3810   3815   3820

266

Asp Arg Glu Ala Leu Leu Ser Arg Leu Ala Ala Leu Ala Asp Gly Arg
825   3830   3835   3840

Thr Ala Pro Gly Val Ile Thr Gly Ser Ala Asn Ser Gly Gly Arg Ile
          3845   3850   3855

Gly Phe Val Phe Ser Gly Gln Gly Ser Gln Trp Leu Gly Met Gly Lys
          3860   3865   3870

Ala Leu Cys Ala Ala Phe Pro Ala Phe Ala Asp Ala Phe Glu Glu Ala
       3875   3880   3885

Cys Asp Ala Leu Ser Ala His Leu Gly Ala Asp Val Arg Gly Val Leu
    3890   3895   3900

Phe Gly Ala Asp Glu Gln Met Leu Asp Arg Thr Leu Trp Ala Gln Ser
905   3910   3915   3920

Gly Ile Phe Ala Val Gln Val Gly Leu Leu Gly Leu Leu Arg Ser Trp
          3925   3930   3935

Gly Val Arg Pro Ala Ala Val Leu Gly His Ser Val Gly Glu Leu Ala
          3940   3945   3950

Ala Ala His Ala Ala Gly Val Leu Ser Leu Pro Asp Ala Ala Arg Leu
    3955   3960   3965

Val Ala Ala Arg Ala His Leu Met Gln Ala Leu Pro Thr Gly Gly Ala
    3970   3975   3980

Met Leu Ala Val Ala Thr Ser Glu Ala Ala Val Gly Pro Leu Leu Ser
985   3990   3995   4000

Gly Val Cys Asp Arg Val Ser Ile Ala Ala Ile Asn Gly Pro Glu Ser
             4005   4010   4015

Val Val Leu Ser Gly Asp Arg Asp Val Leu Val Glu Leu Ala Gly Glu
          4020   4025   4030

Phe Asp Ala Arg Gly Leu Arg Thr Lys Trp Leu Arg Val Ser His Ala
          4035   4040   4045

Phe His Ser His Arg Met Glu Pro Ile Leu Asp Glu Tyr Ala Glu Thr
    4050   4055   4060

Ala Arg Cys Val Glu Phe Gly Glu Pro Val Val Pro Ile Val Ser Ala
065   4070   4075   4080

267

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Ala Thr Gly Ala Leu Asp Thr Thr Gly Leu Met Cys Ala Ala Asp Tyr
          4085              4090              4095

Trp Thr Arg Gln Val Arg Asp Pro Val Arg Phe Gly Asp Gly Val Arg
          4100              4105              4110

Ala Leu Val Gly Gln Gly Val Asp Thr Ile Val Glu Phe Gly Pro Asp
          4115              4120              4125

Gly Ala Leu Ser Ala Leu Val Glu Gln Cys Leu Ala Gly Ser Asp Gln
     4130              4135              4140

Ala Gly Arg Val Ala Ala Ile Pro Leu Met Arg Arg Asp Arg Asp Glu
  145              4150              4155              4160

Val Glu Thr Ala Val Ala Ala Leu Ala His Val His Val Arg Gly Gly
          4165              4170              4175

Ala Val Asp Trp Ser Ala Cys Phe Ala Gly Thr Gly Ala Arg Thr Val
          4180              4185              4190

Glu Leu Pro Thr Tyr Ala Phe Gln Arg Gln Arg Tyr Trp Leu Ala Gly
          4195              4200              4205

Gln Ala Asp Gly Arg Gly Gly Asp Val Val Ala Asp Pro Val Asp Ala
     4210              4215              4220

Arg Phe Trp Glu Leu Val Glu Arg Ala Asp Pro Glu Pro Leu Val Asp
  225              4230              4235              4240

Glu Leu Cys Ile Asp Arg Asp Gln Pro Phe Arg Glu Val Leu Pro Val
          4245              4250              4255

Leu Ala Ser Trp Arg Glu Lys Gln Arg Gln Glu Ala Leu Ala Asp Ser
          4260              4265              4270

Trp Arg Tyr Gln Val Arg Trp Arg Ser Val Glu Val Pro Ser Ala Ala
          4275              4280              4285

Ala Leu Arg Gly Val Trp Leu Val Val Leu Pro Ala Asp Val Pro Arg
     4290              4295              4300

Asp Gln Pro Ala Val Val Ile Asp Ala Leu Ile Ala Arg Gly Ala Glu
  305              4310              4315              4320

Val Ala Val Leu Glu Leu Thr Glu Gln Asp Leu Gln Arg Ser Ala Leu
          4325              4330              4335
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268

Val Asp Lys Val Arg Ala Val Ile Ala Asp Arg Thr Glu Val Thr Gly
        4340   4345   4350

Val Leu Ser Leu Leu Ala Met Asp Gly Met Pro Cys Ala Ala His Pro
        4355   4360   4365

His Leu Ser Arg Gly Val Ala Ala Thr Val Ile Leu Thr Gln Val Leu
     4370   4375   4380

Gly Asp Ala Gly Val Ser Ala Pro Leu Trp Leu Ala Thr Thr Gly Gly
385   4390   4395   4400

Val Glu Ala Gly Thr Glu Asp Gly Pro Ala Asp Pro Asp His Gly Leu
         4405   4410   4415

Ile Trp Gly Leu Gly Arg Val Val Gly Leu Glu His Pro Gln Trp Trp
         4420   4425   4430

Gly Gly Leu Ile Asp Leu Pro Glu Thr Leu Asp Glu Thr Ser Arg Asn
      4435   4440   4445

Gly Leu Val Ala Ala Leu Ala Gly Thr Ala Ala Glu Asp Gln Leu Ala
     4450   4455   4460

Val Arg Ser Ser Gly Leu Phe Val Arg Arg Val Val Arg Ala Ala Arg
465   4470   4475   4480

Asn Pro Arg Ser Glu Thr Trp Arg Ser Arg Gly Thr Val Leu Ile Thr
         4485   4490   4495

Gly Gly Thr Gly Ala Leu Gly Ala Glu Val Ala Arg Trp Leu Ala Arg
         4500   4505   4510

Arg Gly Ala Glu His Leu Val Leu Ile Ser Arg Arg Gly Pro Glu Ala
      4515   4520   4525

Pro Gly Ala Ala Asp Leu Gly Ala Glu Leu Thr Glu Leu Gly Val Lys
      4530   4535   4540

Val Thr Val Leu Ala Cys Asp Val Thr Asp Arg Asp Glu Leu Ala Ala
545   4550   4555   4560

Val Leu Ala Ala Val Pro Thr Glu Tyr Pro Leu Ser Ala Val Val His
         4565   4570   4575

Thr Ala Gly Val Gly Thr Pro Ala Asn Leu Ala Glu Thr Thr Leu Ala
         4580   4585   4590

Gln Phe Ala Asp Val Leu Ser Ala Lys Val Val Gly Ala Ala Asn Leu
    4595   4600   4605

Asp Arg Leu Leu Gly Gly Gln Pro Leu Asp Ala Phe Val Leu Phe Ser
    4610   4615   4620

Ser Ile Ser Gly Val Trp Gly Ala Gly Gly Gln Gly Ala Tyr Ser Ala
625   4630   4635   4640

Ala Asn Ala Tyr Leu Asp Ala Leu Ala Glu Arg Arg Arg Ala Cys Gly
            4645   4650   4655

Arg Pro Ala Thr Cys Ile Ala Trp Gly Pro Trp Ala Gly Ala Gly Met
        4660   4665   4670

Ala Val Gln Glu Gly Asn Glu Ala His Leu Arg Arg Arg Gly Leu Val
    4675   4680   4685

Pro Met Glu Pro Gln Ser Ala Leu Phe Ala Leu Gln Gln Ala Leu Ser
    4690   4695   4700

Gln Arg Glu Thr Ala Ile Thr Val Ala Asp Val Asp Trp Glu Arg Phe
705   4710   4715   4720

Ala Ala Ser Phe Thr Ala Ala Arg Pro Arg Pro Leu Leu Glu Glu Ile
            4725   4730   4735

Val Asp Leu Arg Pro Asp Thr Glu Thr Glu Glu Lys His Gly Ala Gly
            4740   4745   4750

Glu Leu Gly Gln Gln Leu Ala Ala Leu Pro Pro Ala Glu Arg Gly His
        4755   4760   4765

Leu Leu Leu Glu Val Val Leu Ala Glu Thr Ala Ser Thr Leu Gly His
        4770   4775   4780

Asp Ser Ala Glu Ala Val Gln Pro Asp Arg Thr Phe Ala Glu Leu Gly
785   4790   4795   4800

Phe Asp Ser Leu Thr Ala Val Glu Leu Arg Asn Arg Leu Asn Ala Val
            4805   4810   4815

Thr Gly Leu Arg Leu Pro Pro Thr Leu Val Phe Asp His Pro Thr Pro
        4820   4825   4830

Leu Ala Leu Ser Glu Gln Leu Val Pro Ala Leu Val Ala Glu Pro Asp
    4835   4840   4845

270

```
        Asn Gly Ile Glu Ser Leu Leu Ala Glu Leu Asp Arg Leu Asp Thr Thr
            4850            4855            4860


        Leu Ala Gln Gly Pro Ser Ile Pro Leu Glu Asp Gln Ala Lys Val Ala
        865             4870            4875            4880


        Glu Arg Leu His Ala Leu Leu Ala Lys Trp Asp Gly Ala Arg Asp Gly
                    4885            4890            4895


        Thr Ala Arg Ala Thr Ser Pro Gln Ser Leu Thr Ala Ala Thr Asp Asp
                    4900            4905            4910


        Glu Ile Phe Asp Leu Ile Asp Arg Lys Phe Arg Arg
                4915            4920
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<210> 49
<211> 16767
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<400> 49

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atg gcc aat gaa gaa aag ctc cgc gag tac ctc aag cgt gtc gtc gtc      48
Met Ala Asn Glu Glu Lys Leu Arg Glu Tyr Leu Lys Arg Val Val Val
 1               5                   10                  15


gaa ctg gaa gag gcg cac gaa cgc ctg cac gag ttg gag cgc cag gag      96
Glu Leu Glu Glu Ala His Glu Arg Leu His Glu Leu Glu Arg Gln Glu
                20                  25                  30


cac gac ccc atc gcg atc gtg tcg atg gga tgt cgt tat ccc ggt ggc     144
His Asp Pro Ile Ala Ile Val Ser Met Gly Cys Arg Tyr Pro Gly Gly
            35                  40                  45


gtc tcc act ccg gag gag ctg tgg cga ctg gtc gtc gac gga gga gac     192
Val Ser Thr Pro Glu Glu Leu Trp Arg Leu Val Val Asp Gly Gly Asp
        50                  55                  60


gcg atc gcg aac ttc ccc gaa gac cgt ggc tgg aat ctg gac gag ctg     240
Ala Ile Ala Asn Phe Pro Glu Asp Arg Gly Trp Asn Leu Asp Glu Leu
65                  70                  75                  80
```

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ttc gat cct gat ccg ggc cga gcc ggg acc tcc tac gtc cgc gag ggt    288
Phe Asp Pro Asp Pro Gly Arg Ala Gly Thr Ser Tyr Val Arg Glu Gly
                 85                  90                  95

ggt ttc ctg cgc ggg gtc gcg gac ttc gat gcc ggg ctc ttc ggg atc    336
Gly Phe Leu Arg Gly Val Ala Asp Phe Asp Ala Gly Leu Phe Gly Ile
             100                 105                 110

agt ccg cgc gag gca cag gcg atg gac ccg caa cag cgg ttg ctg ctg    384
Ser Pro Arg Glu Ala Gln Ala Met Asp Pro Gln Gln Arg Leu Leu Leu
             115                 120                 125

gag atc tcg tgg gag gtg ttc gag cgc gcc ggc att gac ccg ttt tct    432
Glu Ile Ser Trp Glu Val Phe Glu Arg Ala Gly Ile Asp Pro Phe Ser
             130                 135                 140

ttg cgg ggt acc aag acc ggt gtg ttc gcg ggc ctg atc tac cac gac    480
Leu Arg Gly Thr Lys Thr Gly Val Phe Ala Gly Leu Ile Tyr His Asp
145                 150                 155                 160

tac gcg tcg cgg ttt cgc aag acc ccc gcg gag ttc gag ggt tac ttc    528
Tyr Ala Ser Arg Phe Arg Lys Thr Pro Ala Glu Phe Glu Gly Tyr Phe
             165                 170                 175

gcc acc ggc aac gcg ggc agc gtc gca tcc ggc cgg gtg gct tac acc    576
Ala Thr Gly Asn Ala Gly Ser Val Ala Ser Gly Arg Val Ala Tyr Thr
             180                 185                 190

ttc ggg tta gag ggc ccg gcg gtc acc gtg gac acc gcc tgc tcg tcg    624
Phe Gly Leu Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser
             195                 200                 205

tcc ctg gtg gcg ctg cac ctg gcc tgc cag tcc ctg cgg ctg ggc gaa    672
Ser Leu Val Ala Leu His Leu Ala Cys Gln Ser Leu Arg Leu Gly Glu
             210                 215                 220

tgc gac ctg gcc ctg gcc ggt ggc att tcg gtg atg gcc acg ccg gga    720
Cys Asp Leu Ala Leu Ala Gly Gly Ile Ser Val Met Ala Thr Pro Gly
225                 230                 235                 240

gcc ttc gtc gag ttc agc cgg caa cgc gca ctc gcc tcg gat ggc cgg    768
Ala Phe Val Glu Phe Ser Arg Gln Arg Ala Leu Ala Ser Asp Gly Arg
             245                 250                 255

tgc aag ccc ttc gcg gat gcc gcc gac ggc acc ggc tgg ggc gag ggc    816
Cys Lys Pro Phe Ala Asp Ala Ala Asp Gly Thr Gly Trp Gly Glu Gly
             260                 265                 270
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272

```
gcc gga atg ctg ctg ctg gaa cgg ctg tcg gac gca cga cga aac ggc     864
Ala Gly Met Leu Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly
            275                 280                 285

cac ccg gtg ctg gcg gcg gtg gtc ggt tcc gcg atc aac cag gac ggg     912
His Pro Val Leu Ala Ala Val Val Gly Ser Ala Ile Asn Gln Asp Gly
            290                 295                 300

acg tcc aac ggc ctg acc gcg ccc agc ggt ccc gca cag cag cga gtg     960
Thr Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ala Gln Gln Arg Val
305                 310                 315                 320

atc cgc caa gcc ctg gcg aac gcc ggg ttg tcg ccc gcc gag gtc gat    1008
Ile Arg Gln Ala Leu Ala Asn Ala Gly Leu Ser Pro Ala Glu Val Asp
                325                 330                 335

gtg gtc gag gcg cac ggc acg ggc acg gcc ttg ggc gac ccg atc gag    1056
Val Val Glu Ala His Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu
                340                 345                 350

gcg cag gcc ctg atc gcc acc tac ggg gcg aac cgg tcg gcg gat cat    1104
Ala Gln Ala Leu Ile Ala Thr Tyr Gly Ala Asn Arg Ser Ala Asp His
                355                 360                 365

ccg ctg ctg ctg ggt tcc ctc aag tcg aac atc ggc cac acc cag gct    1152
Pro Leu Leu Leu Gly Ser Leu Lys Ser Asn Ile Gly His Thr Gln Ala
            370                 375                 380

gcc gcc ggt gtg gcc ggg gtg atc aag tcg gtc ctg gcc atc agg cac    1200
Ala Ala Gly Val Ala Gly Val Ile Lys Ser Val Leu Ala Ile Arg His
385                 390                 395                 400

cgg gag atg ccc cgc agc ctg cac atc gac cag cca tcg cag cac gtg    1248
Arg Glu Met Pro Arg Ser Leu His Ile Asp Gln Pro Ser Gln His Val
                405                 410                 415

gac tgg tcg gcg ggc gcg gtg cgg ctg ctc acg gac agc gtt gac tgg    1296
Asp Trp Ser Ala Gly Ala Val Arg Leu Leu Thr Asp Ser Val Asp Trp
            420                 425                 430

ccg gat ctc ggc agg ccg cgc cga gca ggg gtg tcc tcg ttc ggc atg    1344
Pro Asp Leu Gly Arg Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Met
            435                 440                 445

agc ggt acc aac gca cac ctg atc gtc gag gaa gta tcc gac gag ccg    1392
Ser Gly Thr Asn Ala His Leu Ile Val Glu Glu Val Ser Asp Glu Pro
            450                 455                 460
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gtc tcg ggc agt acc gag ccg acc ggg gca ttt ccc tgg ccg ctg tcc      1440
Val Ser Gly Ser Thr Glu Pro Thr Gly Ala Phe Pro Trp Pro Leu Ser
465             470             475             480


ggc aag acg gag acg gca ttg cgc gag cag gct gcc gag ttg ctc tcc      1488
Gly Lys Thr Glu Thr Ala Leu Arg Glu Gln Ala Ala Glu Leu Leu Ser
                485             490             495


gta gtg acc gag cac ccg gag ccg gga ctg ggg gac gtc ggg tac tcg      1536
Val Val Thr Glu His Pro Glu Pro Gly Leu Gly Asp Val Gly Tyr Ser
                500             505             510


ctg gcc acc ggt cgc gct gcg atg gag cac cgg gct gtc gtg gtt gcc      1584
Leu Ala Thr Gly Arg Ala Ala Met Glu His Arg Ala Val Val Val Ala
            515             520             525


gac gat cgg gac tct ttc gtc gcc gga ctg acg gcg ttg gct gcg ggc      1632
Asp Asp Arg Asp Ser Phe Val Ala Gly Leu Thr Ala Leu Ala Ala Gly
        530             535             540


gtt ccg gca gcc aac gtg gtg cag ggc gcg gcc gac tgc aag gga aag      1680
Val Pro Ala Ala Asn Val Val Gln Gly Ala Ala Asp Cys Lys Gly Lys
545             550             555             560


gtc gcg ttc gtg ttc ccc ggc cag ggc tcg cat tgg cag ggg atg gcg      1728
Val Ala Phe Val Phe Pro Gly Gln Gly Ser His Trp Gln Gly Met Ala
                565             570             575


agg gaa ctg tcc gaa tcc tcg ccg gtg ttc cgg cgg aag ctg gcg gaa      1776
Arg Glu Leu Ser Glu Ser Ser Pro Val Phe Arg Arg Lys Leu Ala Glu
                580             585             590


tgc gcg gcg gct acg gcc cct tac gtg gac tgg tcg ctg ctc ggc gtc      1824
Cys Ala Ala Ala Thr Ala Pro Tyr Val Asp Trp Ser Leu Leu Gly Val
            595             600             605


ctt cgc ggt gat ccc gat gca ccc gcg ctg gat cgc gac gac gtg att      1872
Leu Arg Gly Asp Pro Asp Ala Pro Ala Leu Asp Arg Asp Asp Val Ile
        610             615             620


cag ctc gcg ctg ttc gcc atg atg gtg tcg ctg gcc gaa ctg tgg cgt      1920
Gln Leu Ala Leu Phe Ala Met Met Val Ser Leu Ala Glu Leu Trp Arg
625             630             635             640


tcg tgc gga gtg gag ccc gcc gcg gtg gtc ggt cat tcc cag ggc gag      1968
Ser Cys Gly Val Glu Pro Ala Ala Val Val Gly His Ser Gln Gly Glu
                645             650             655
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274

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atc gcc gcc gcc cat gtg gca ggc gct ttg tcc ttg act gat gcg gtg    2016
Ile Ala Ala Ala His Val Ala Gly Ala Leu Ser Leu Thr Asp Ala Val
            660                 665                 670

cgc atc atc gct gcc cgc tgc gat gcg gtg tcg gcg ctg acc ggg aag    2064
Arg Ile Ile Ala Ala Arg Cys Asp Ala Val Ser Ala Leu Thr Gly Lys
            675                 680                 685

gga ggc atg ctc gcg att gcc ttg ccg gaa agc gcg gtg gtg aag cga    2112
Gly Gly Met Leu Ala Ile Ala Leu Pro Glu Ser Ala Val Val Lys Arg
            690                 695                 700

atc gca ggc ctg ccg gag ctg acc gtt gcg gcg gtc aac gga ccc ggc    2160
Ile Ala Gly Leu Pro Glu Leu Thr Val Ala Ala Val Asn Gly Pro Gly
705                 710                 715                 720

tcc act gtc gtt tcc ggc gaa ccg tcg gct ctg gag cgt ctg cag acc    2208
Ser Thr Val Val Ser Gly Glu Pro Ser Ala Leu Glu Arg Leu Gln Thr
                    725                 730                 735

gaa ctg acc gcg gaa aac gtg cag acc cgg cgg gtg gga att gat tac    2256
Glu Leu Thr Ala Glu Asn Val Gln Thr Arg Arg Val Gly Ile Asp Tyr
            740                 745                 750

gcc tcg cat tcg ccg cag atc gcg cag gtc cag ggc cgg ctt ctg gac    2304
Ala Ser His Ser Pro Gln Ile Ala Gln Val Gln Gly Arg Leu Leu Asp
            755                 760                 765

cgg ctg ggc gaa gtc ggg tcc gaa cct gct gag atc gct ttc tac tcg    2352
Arg Leu Gly Glu Val Gly Ser Glu Pro Ala Glu Ile Ala Phe Tyr Ser
            770                 775                 780

acg gtc acc ggc gag cgg acg gac acc ggc cga ctc gac gcc gac tac    2400
Thr Val Thr Gly Glu Arg Thr Asp Thr Gly Arg Leu Asp Ala Asp Tyr
785                 790                 795                 800

tgg tac cag aac ctt cgg cag ccc gtc cgc ttc cag cag acc gtc gcc    2448
Trp Tyr Gln Asn Leu Arg Gln Pro Val Arg Phe Gln Gln Thr Val Ala
                    805                 810                 815

cgg atg gca gat cag ggc tat cgg ttc ttc gtc gag gtg agc ccg cac    2496
Arg Met Ala Asp Gln Gly Tyr Arg Phe Phe Val Glu Val Ser Pro His
            820                 825                 830

ccg ctg ctc acc gcc gga atc cag gaa acg ctg gaa gcc gcg gac gcg    2544
Pro Leu Leu Thr Ala Gly Ile Gln Glu Thr Leu Glu Ala Ala Asp Ala
            835                 840                 845
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ggc ggg gtg gtg gtc ggt tcg ctg cgg cgt ggc gag ggc ggc tcc cgg    2592
Gly Gly Val Val Val Gly Ser Leu Arg Arg Gly Glu Gly Gly Ser Arg
    850             855             860

cgc tgg ctg act tcg ctg gcc gag tgc cag gtg cgc gga ctg ccg gtg    2640
Arg Trp Leu Thr Ser Leu Ala Glu Cys Gln Val Arg Gly Leu Pro Val
865             870             875             880

aat tgg gaa cag gta ttc ctc aac acc gga gcc cga cgc gtg ccg ctg    2688
Asn Trp Glu Gln Val Phe Leu Asn Thr Gly Ala Arg Arg Val Pro Leu
            885             890             895

ccg acc tac ccg ttc cag cgg cag cgg tac tgg ttg gag tcc gcc gag    2736
Pro Thr Tyr Pro Phe Gln Arg Gln Arg Tyr Trp Leu Glu Ser Ala Glu
            900             905             910

tac gac gcg ggc gat ctc ggt tcg gtg ggc ttg ctc tcc gcc gag cat    2784
Tyr Asp Ala Gly Asp Leu Gly Ser Val Gly Leu Leu Ser Ala Glu His
            915             920             925

ccc ctg ctc ggg gct gcg gtg acg ctg gcc gat gcg ggc ggg ttc ctg    2832
Pro Leu Leu Gly Ala Ala Val Thr Leu Ala Asp Ala Gly Gly Phe Leu
    930             935             940

ctg acc ggc aag ctg tcg gtc aag acc cag ccc tgg ttg gcc gac cac    2880
Leu Thr Gly Lys Leu Ser Val Lys Thr Gln Pro Trp Leu Ala Asp His
945             950             955             960

gtg gtc ggc ggg gcg atc ctg ctg ccc ggc acc gcg ttc gtg gaa atg    2928
Val Val Gly Gly Ala Ile Leu Leu Pro Gly Thr Ala Phe Val Glu Met
            965             970             975

ctg ata cgc gcc gcg gac cag gtc ggg tgc gat ctg atc gag gag ttg    2976
Leu Ile Arg Ala Ala Asp Gln Val Gly Cys Asp Leu Ile Glu Glu Leu
            980             985             990

tcc ctg acg act ccg ctg gtt ttg ccc gcg acc ggt gcg gtg cag gtg    3024
Ser Leu Thr Thr Pro Leu Val Leu Pro Ala Thr Gly Ala Val Gln Val
        995             1000            1005

cag atc gcg gtt ggc ggt ccg gac gag gcc ggg cgc cgc tcg gtc cgc    3072
Gln Ile Ala Val Gly Gly Pro Asp Glu Ala Gly Arg Arg Ser Val Arg
    1010            1015            1020

gtg cat tcc tgt cga gac gac gcc gtg ccg cag gac tcg tgg acc tgc    3120
Val His Ser Cys Arg Asp Asp Ala Val Pro Gln Asp Ser Trp Thr Cys
1025            1030            1035            1040
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cac gcg acc ggc acg ttg acc tcc agc gat cac cag gac gcc ggc cag    3168
His Ala Thr Gly Thr Leu Thr Ser Ser Asp His Gln Asp Ala Gly Gln
              1045               1050               1055

ggc ccc gat ggg att tgg ccg ccc aac gat gct gtc gcg gtt ccg ctg    3216
Gly Pro Asp Gly Ile Trp Pro Pro Asn Asp Ala Val Ala Val Pro Leu
              1060               1065               1070

gac agc ttc tac gcc cgc gca gct gag cgg ggc ttc gat ttc ggc ccg    3264
Asp Ser Phe Tyr Ala Arg Ala Ala Glu Arg Gly Phe Asp Phe Gly Pro
              1075               1080               1085

gcg ttc cag ggg ttg cag gcg gct tgg aag cgc gga gac gag atc ttc    3312
Ala Phe Gln Gly Leu Gln Ala Ala Trp Lys Arg Gly Asp Glu Ile Phe
              1090               1095               1100

gcc gag gtc ggc ctg ccc acc gca cac cgc gaa gac gcc ggc agg ttc    3360
Ala Glu Val Gly Leu Pro Thr Ala His Arg Glu Asp Ala Gly Arg Phe
1105               1110               1115               1120

gga atc cac cct gct ctg ctg gat gcg gca ctg cag gcg ctg ggc gca    3408
Gly Ile His Pro Ala Leu Leu Asp Ala Ala Leu Gln Ala Leu Gly Ala
                  1125               1130               1135

gcc gaa gag gat ccg gac gag gga tgg ctc ccg ttc gcg tgg caa ggt    3456
Ala Glu Glu Asp Pro Asp Glu Gly Trp Leu Pro Phe Ala Trp Gln Gly
              1140               1145               1150

gtg tcc ctc aaa gcg acg ggc gca ctt tcc ctt cgg gtg cac ctc gtt    3504
Val Ser Leu Lys Ala Thr Gly Ala Leu Ser Leu Arg Val His Leu Val
              1155               1160               1165

ccg gcg ggc gcg aat gcg gtg tcg gtg ttc acg acc gac acg act ggc    3552
Pro Ala Gly Ala Asn Ala Val Ser Val Phe Thr Thr Asp Thr Thr Gly
              1170               1175               1180

caa gcc gtg ctc tcc atc gat tcg ctg gtg ctg cgc cag att tcg gac    3600
Gln Ala Val Leu Ser Ile Asp Ser Leu Val Leu Arg Gln Ile Ser Asp
1185               1190               1195               1200

aag cag ttg gca gcg gcc cgt gcg atg gaa cac gag tcc ctg ttc cgg    3648
Lys Gln Leu Ala Ala Ala Arg Ala Met Glu His Glu Ser Leu Phe Arg
              1205               1210               1215

gtc gac tgg aag cga atc tcg ccc ggc gct gcc aag ccg gtc tcc tgg    3696
Val Asp Trp Lys Arg Ile Ser Pro Gly Ala Ala Lys Pro Val Ser Trp
              1220               1225               1230
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gca gtg atc ggc aat gac gaa ctc gcc cga gcc tgc ggc tcg gca ctt    3744
Ala Val Ile Gly Asn Asp Glu Leu Ala Arg Ala Cys Gly Ser Ala Leu
         1235            1240            1245


ggc acg gaa ctc cac ccc gac ctg acc ggg ttg gct gac ccg ccc ccg    3792
Gly Thr Glu Leu His Pro Asp Leu Thr Gly Leu Ala Asp Pro Pro Pro
     1250            1255            1260


gac gtc gtg gtg gtg cca tgc ggt gcg tct cgc cag gac ttg gac gtt    3840
Asp Val Val Val Val Pro Cys Gly Ala Ser Arg Gln Asp Leu Asp Val
 1265            1270            1275            1280


gct tcc gag gca cgt gcc gcg aca caa cgc atg ctt gac ctg atc cag    3888
Ala Ser Glu Ala Arg Ala Ala Thr Gln Arg Met Leu Asp Leu Ile Gln
             1285            1290            1295


gat tgg ttg gcg gcg gcg cga ttc gcc gga tct cgc ctg gtg gtt gtg    3936
Asp Trp Leu Ala Ala Ala Arg Phe Ala Gly Ser Arg Leu Val Val Val
             1300            1305            1310


acg tgt ggt gcg gcg tcg aca ggt ccc gcc gag ggt gtt tcc gac ctg    3984
Thr Cys Gly Ala Ala Ser Thr Gly Pro Ala Glu Gly Val Ser Asp Leu
         1315            1320            1325


gtg cat gct gcg tcg tgg ggt ttg ttg cgt tcg gcg cag tcg gag aac    4032
Val His Ala Ala Ser Trp Gly Leu Leu Arg Ser Ala Gln Ser Glu Asn
 1330            1335            1340


ccg gac cga ttc gtg ttg gtc gat gtg gac gga acc gcc gaa tca tgg    4080
Pro Asp Arg Phe Val Leu Val Asp Val Asp Gly Thr Ala Glu Ser Trp
1345            1350            1355            1360


cgt gcg ctc gcg gcg gcc gtg cgt tcc gga gaa ccg cag ctg gcg ttg    4128
Arg Ala Leu Ala Ala Ala Val Arg Ser Gly Glu Pro Gln Leu Ala Leu
             1365            1370            1375


cgc gcc ggt gaa gtc cgg gtg cct cgc ctg gcg cga tgt gtt gcc gcc    4176
Arg Ala Gly Glu Val Arg Val Pro Arg Leu Ala Arg Cys Val Ala Ala
             1380            1385            1390


gag gac agc cgg atc cca gtg ccc ggt gcg gat ggg acg gtg ttg att    4224
Glu Asp Ser Arg Ile Pro Val Pro Gly Ala Asp Gly Thr Val Leu Ile
         1395            1400            1405


tcc ggc ggt acg ggc ctg ctg ggc ggg ttg gtt gcc cgg cat ttg gtg    4272
Ser Gly Gly Thr Gly Leu Leu Gly Gly Leu Val Ala Arg His Leu Val
 1410            1415            1420
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gcg gag cgc ggt gtc cgc cgc ctg gtg ctc gcg ggg cga cgc ggc tgg   4320
Ala Glu Arg Gly Val Arg Arg Leu Val Leu Ala Gly Arg Arg Gly Trp
1425   1430   1435   1440

agc gcc ccc ggg gtc acc gac ctg gtg gat gag ttg gtg ggc ctg gga   4368
Ser Ala Pro Gly Val Thr Asp Leu Val Asp Glu Leu Val Gly Leu Gly
                1445   1450   1455

gct gcg gtc gag gtg gcg agc tgc gat gtc ggg gat cgg gcc cag ttg   4416
Ala Ala Val Glu Val Ala Ser Cys Asp Val Gly Asp Arg Ala Gln Leu
            1460   1465   1470

gac cgg ctg ctg acg acg atc tcg gca gag ttc ccg ctg cgc gga gtg   4464
Asp Arg Leu Leu Thr Thr Ile Ser Ala Glu Phe Pro Leu Arg Gly Val
            1475   1480   1485

gtg cat gcg gcc ggg gca ctt gcc gac ggg gtc gtc gag tcg ctg aca   4512
Val His Ala Ala Gly Ala Leu Ala Asp Gly Val Val Glu Ser Leu Thr
        1490   1495   1500

cca gag cac gtg gca aag gtg ttc ggc ccg aag gcc gcc ggt gcg tgg   4560
Pro Glu His Val Ala Lys Val Phe Gly Pro Lys Ala Ala Gly Ala Trp
1505   1510   1515   1520

cac ctg cac gag ttg act ctt gat ctg gat ctc tcg ttc ttc gtg ctc   4608
His Leu His Glu Leu Thr Leu Asp Leu Asp Leu Ser Phe Phe Val Leu
                1525   1530   1535

ttc tcc tcg ttc tcc ggc gtg gcg ggg gct gcg ggt cag gga aac tac   4656
Phe Ser Ser Phe Ser Gly Val Ala Gly Ala Ala Gly Gln Gly Asn Tyr
            1540   1545   1550

gcg gcg gcg aac gcg ttc ctg gac ggc ctg gct cag cac cgg cgg acg   4704
Ala Ala Ala Asn Ala Phe Leu Asp Gly Leu Ala Gln His Arg Arg Thr
        1555   1560   1565

gcg ggg ctg cct gcg gtg tcg ctg gct tgg ggc ttg tgg gag cag ccc   4752
Ala Gly Leu Pro Ala Val Ser Leu Ala Trp Gly Leu Trp Glu Gln Pro
    1570   1575   1580

agc ggg atg acc gga gcg ctc gat gcg gcg ggc cgt agc cgc att gcg   4800
Ser Gly Met Thr Gly Ala Leu Asp Ala Ala Gly Arg Ser Arg Ile Ala
1585   1590   1595   1600

cgc acc aat ccg ccg atg tcc gcg ccg gac ggg ttg cgg ctg ttc gag   4848
Arg Thr Asn Pro Pro Met Ser Ala Pro Asp Gly Leu Arg Leu Phe Glu
                1605   1610   1615

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atg gcg ttt cgc gtt ccg ggc gaa tcg ctt ctg gtt ccg gtc cac gtc    4896
Met Ala Phe Arg Val Pro Gly Glu Ser Leu Leu Val Pro Val His Val
            1620                1625                1630


gac ctg aac gcc ctg cgc gct gat gcg gcc gac ggc ggt gtg cct gcg    4944
Asp Leu Asn Ala Leu Arg Ala Asp Ala Ala Asp Gly Gly Val Pro Ala
            1635                1640                1645


ttg ttg cgc gac ctg gtg cca gcg ccc gtg cgg cgg agc gcg gtc aac    4992
Leu Leu Arg Asp Leu Val Pro Ala Pro Val Arg Arg Ser Ala Val Asn
        1650                1655                1660


gag tcg gcg gac gtc aac ggt ctg gtt ggt cgg ctg cgg agg ctg ccg    5040
Glu Ser Ala Asp Val Asn Gly Leu Val Gly Arg Leu Arg Arg Leu Pro
1665                1670                1675                1680


gac ctg gat cag gaa acc cag ctg ttg ggt ttg gtg cgc gag cat gtt    5088
Asp Leu Asp Gln Glu Thr Gln Leu Leu Gly Leu Val Arg Glu His Val
                1685                1690                1695


tcg gcg gtg ctg ggg cat tcg ggt gcg gtc gag gtc ggg gcc gat cgt    5136
Ser Ala Val Leu Gly His Ser Gly Ala Val Glu Val Gly Ala Asp Arg
                1700                1705                1710


gct ttc cgg gat ttg ggt ttt gat tcg ttg tcc ggt gtg gag ttt cgg    5184
Ala Phe Arg Asp Leu Gly Phe Asp Ser Leu Ser Gly Val Glu Phe Arg
            1715                1720                1725


aac cgg ctt ggc ggg gtg ctg ggc gtt cgg ttg ccg gct act gcg gtg    5232
Asn Arg Leu Gly Gly Val Leu Gly Val Arg Leu Pro Ala Thr Ala Val
        1730                1735                1740


ttc gac tat ccg aca ccg cgg gcg ttg gtt cgg ttc ttg ctc gac aaa    5280
Phe Asp Tyr Pro Thr Pro Arg Ala Leu Val Arg Phe Leu Leu Asp Lys
1745                1750                1755                1760


ctg att ggt ggc gtg gag gct ccg act ccc gca ccg gcg gct gtg gcg    5328
Leu Ile Gly Gly Val Glu Ala Pro Thr Pro Ala Pro Ala Ala Val Ala
                1765                1770                1775


gcg gtg act gct gac gat ccc gtt gtg atc gtg ggg atg ggc tgt cgt    5376
Ala Val Thr Ala Asp Asp Pro Val Val Ile Val Gly Met Gly Cys Arg
            1780                1785                1790


tat ccg ggt ggg gtg tcc tcg ccg gag gag ctt tgg cgt ttg gtg gcc    5424
Tyr Pro Gly Gly Val Ser Ser Pro Glu Glu Leu Trp Arg Leu Val Ala
        1795                1800                1805
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ggg ggc ttg gat gcg gtg gcg gag ttc ccg gac gat cgt ggc tgg gat   5472
Gly Gly Leu Asp Ala Val Ala Glu Phe Pro Asp Asp Arg Gly Trp Asp
 1810   1815   1820

cag gcg ggg ttg ttc gat ccg gat ccc gat cgt ctt ggg·acc tcg tat   5520
Gln Ala Gly Leu Phe Asp Pro Asp Pro Asp Arg Leu Gly Thr Ser Tyr
 1825   1830   1835   1840

gtg tgt gag ggt ggc ttc ctg cga gat gcg gca gag ttc gat gcc ggt   5568
Val Cys Glu Gly Gly Phe Leu Arg Asp Ala Ala Glu Phe Asp Ala Gly
             1845   1850   1855

ttc ttc ggg att tcc ccg cgt gag gcg ttg gcg atg gat ccg cag cag   5616
Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln
         1860   1865   1870

cgg ttg ctg ctg gaa gtc gct tgg gaa acc gtg gag cgg gcg ggg att   5664
Arg Leu Leu Leu Glu Val Ala Trp Glu Thr Val Glu Arg Ala Gly Ile
         1875   1880   1885

gat ccg ctt tcg ttg cgg ggg agc cgg acc ggc gtg ttc gcg ggg ctg   5712
Asp Pro Leu Ser Leu Arg Gly Ser Arg Thr Gly Val Phe Ala Gly Leu
     1890   1895   1900

atg cac cac gac tac ggc gcg cgg ttc atc acg agg gcg ccg gag ggt   5760
Met His His Asp Tyr Gly Ala Arg Phe Ile Thr Arg Ala Pro Glu Gly
 1905   1910   1915   1920

ttc gag ggt tat cta ggt aat ggc agc gcg gga ggc gtg ttt tcg ggt   5808
Phe Glu Gly Tyr Leu Gly Asn Gly Ser Ala Gly Gly Val Phe Ser Gly
             1925   1930   1935

cgg gtt gcg tat tcg ttt ggt ttc gag ggt cct gcg gtg acg gtg gat   5856
Arg Val Ala Tyr Ser Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp
         1940   1945   1950

acg gcg tgt tcg tcg tcg ttg gtg gcg ctg cac ctg gcg ggt caa gca   5904
Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala Gly Gln Ala
         1955   1960   1965

ctg cgg tct ggt gag tgt gat ctg gct ctt gcg ggt ggt gtg acg gtg   5952
Leu Arg Ser Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val
     1970   1975   1980

atg gcc acg ccg ggg atg ttc gtg gag ttt tcg cgt caa cgg ggc ttg   6000
Met Ala Thr Pro Gly Met Phe Val Glu Phe Ser Arg Gln Arg Gly Leu
 1985   1990   1995   2000

                                     281

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gcg gcg gat ggg cgg tgc aag tcg ttt gcg gcg gct gcg gat ggc acc    6048
Ala Ala Asp Gly Arg Cys Lys Ser Phe Ala Ala Ala Ala Asp Gly Thr
         2005              2010              2015


ggt tgg gga gaa ggc gcg ggc ttg gtg ttg ttg gag cgg ctg tcg gat    6096
Gly Trp Gly Glu Gly Ala Gly Leu Val Leu Leu Glu Arg Leu Ser Asp
         2020              2025              2030


gcc cgg cgc aac ggg cac gcg gtt ctg gcg gtc gtg cgg ggt agc gcg    6144
Ala Arg Arg Asn Gly His Ala Val Leu Ala Val Val Arg Gly Ser Ala
         2035              2040              2045


gtg aat cag gat ggt gcg tcg aat ggt ttg acg gcg ccg aat ggg ccc    6192
Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro
         2050              2055              2060


tcg cag cag cgg gtg atc acg cag gcg ttg gcg agt gct ggt ttg tcg    6240
Ser Gln Gln Arg Val Ile Thr Gln Ala Leu Ala Ser Ala Gly Leu Ser
2065              2070              2075              2080


gtg tct gat gtg gac gcc gtg gag gcg cat ggg act gga acc agg ctt    6288
Val Ser Asp Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu
         2085              2090              2095


ggt gat ccg att gag gcg cag gct ctg att gcc act tac ggg cag ggg    6336
Gly Asp Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr Tyr Gly Gln Gly
         2100              2105              2110


cgg gat agc gat cgg ccg ttg tgg ttg ggg tcg gtg aag tcg aat att    6384
Arg Asp Ser Asp Arg Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile
         2115              2120              2125


ggt cat acg cag gcg gcg gcg ggt gtc gct ggt gtg atc aag atg gtg    6432
Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val
         2130              2135              2140


atg gcg atg cgg cac ggg cag ctg ccc gcg acg ttg cat gtg gat gaa    6480
Met Ala Met Arg His Gly Gln Leu Pro Ala Thr Leu His Val Asp Glu
2145              2150              2155              2160


cct acg tcg gaa gtg gat tgg tcg gcg ggg gat gtc cag ctc ctc acg    6528
Pro Thr Ser Glu Val Asp Trp Ser Ala Gly Asp Val Gln Leu Leu Thr
         2165              2170              2175


gag aac acc ccc tgg ccc ggc aac agc cat cct cgg cgg gtg ggc gtg    6576
Glu Asn Thr Pro Trp Pro Gly Asn Ser His Pro Arg Arg Val Gly Val
         2180              2185              2190
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282

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tcg tcg ttc ggg atc agc ggc acc aac gca cac gtc atc ctc gaa caa   6624
Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Val Ile Leu Glu Gln
        2195             2200             2205

gcc tcg aaa aca cca gac gag act gcg gac aag agc ggt ccc gat tcg   6672
Ala Ser Lys Thr Pro Asp Glu Thr Ala Asp Lys Ser Gly Pro Asp Ser
        2210             2215             2220

gaa tcg acc gtg gac ctt cca gcg gtc ccg ttg atc gtg tcg ggg aga   6720
Glu Ser Thr Val Asp Leu Pro Ala Val Pro Leu Ile Val Ser Gly Arg
2225             2230             2235             2240

aca ccg gca gcg ctc agc gct cag gcg agc gca ttg ttg tcc tat ttg   6768
Thr Pro Ala Ala Leu Ser Ala Gln Ala Ser Ala Leu Leu Ser Tyr Leu
            2245             2250             2255

ggt gag cgt ggc gat att tcc acg ctg gat gcg gcg ttt tcg ttg gct   6816
Gly Glu Arg Gly Asp Ile Ser Thr Leu Asp Ala Ala Phe Ser Leu Ala
            2260             2265             2270

tcc tcc cgg gcc gcg ttg gag gag cgg gcg gtg gtg ctg gga gcg gac   6864
Ser Ser Arg Ala Ala Leu Glu Glu Arg Ala Val Val Leu Gly Ala Asp
        2275             2280             2285

cgc gaa acg ttg ttg tcc ggg ttg gaa gcg ctg gct tcc ggt cgc gag   6912
Arg Glu Thr Leu Leu Ser Gly Leu Glu Ala Leu Ala Ser Gly Arg Glu
        2290             2295             2300

gct tct ggg gtg gtg tcg gga tcc ccg gtc tct ggc ggg gtt ggg ttc   6960
Ala Ser Gly Val Val Ser Gly Ser Pro Val Ser Gly Gly Val Gly Phe
2305             2310             2315             2320

gtg ttc gcc ggt cag ggc gga cag tgg ttg ggg atg ggc cgg ggg ctc   7008
Val Phe Ala Gly Gln Gly Gly Gln Trp Leu Gly Met Gly Arg Gly Leu
            2325             2330             2335

tac tcg gtt ttt ccg gtg ttc gct gac gcg ttt gac gaa gca tgt gcc   7056
Tyr Ser Val Phe Pro Val Phe Ala Asp Ala Phe Asp Glu Ala Cys Ala
            2340             2345             2350

gga ctg gac gcg cat ctg ggg cag gac gtg ggg gtc cgg gat gtg gtg   7104
Gly Leu Asp Ala His Leu Gly Gln Asp Val Gly Val Arg Asp Val Val
        2355             2360             2365

ttt ggt tcc gac ggg tcc ttg ttg gat cgg acg ctg tgg gcc cag tcg   7152
Phe Gly Ser Asp Gly Ser Leu Leu Asp Arg Thr Leu Trp Ala Gln Ser
        2370             2375             2380
```

ggt ttg ttc gcg ttg cag gtt ggt ttg ctg agc ctg ctg ggt tcg tgg   7200
Gly Leu Phe Ala Leu Gln Val Gly Leu Leu Ser Leu Leu Gly Ser Trp
2385   2390   2395   2400

ggt gtc cgg ccg ggt gtg gtg ctg ggc cat tcg gtc ggc gag ttc gcg   7248
Gly Val Arg Pro Gly Val Val Leu Gly His Ser Val Gly Glu Phe Ala
               2405   2410   2415

gcg gcg gtt gcg gcg gga gtg ttg tcg ttg ccg gat gcg gct cgg atg   7296
Ala Ala Val Ala Ala Gly Val Leu Ser Leu Pro Asp Ala Ala Arg Met
               2420   2425   2430

gtg gcg ggt cgt gcc cgg ttg atg cag gcg ttg cct tct ggc ggt gcc   7344
Val Ala Gly Arg Ala Arg Leu Met Gln Ala Leu Pro Ser Gly Gly Ala
               2435   2440   2445

atg ttg gcg gtg gct gct ggt gag gag cag ctg cgg ccg ttg ttg gcc   7392
Met Leu Ala Val Ala Ala Gly Glu Glu Gln Leu Arg Pro Leu Leu Ala
               2450   2455   2460

gat cgg gtt gat ggt gcg ggt atc gcc gcg gtc aac gct cct gag tcg   7440
Asp Arg Val Asp Gly Ala Gly Ile Ala Ala Val Asn Ala Pro Glu Ser
2465   2470   2475   2480

gtg gtg ctc tcc ggc gat cgg gag gtg ctt gac gac atc gcc ggc gcg   7488
Val Val Leu Ser Gly Asp Arg Glu Val Leu Asp Asp Ile Ala Gly Ala
               2485   2490   2495

ctg gat ggg caa ggg att cgg tgg cgg cgg ttg cgg gtt tcg cat gcg   7536
Leu Asp Gly Gln Gly Ile Arg Trp Arg Arg Leu Arg Val Ser His Ala
               2500   2505   2510

ttt cat tcg tat cgg atg gac ccg atg ttg cag gag ttc gcc gaa atc   7584
Phe His Ser Tyr Arg Met Asp Pro Met Leu Gln Glu Phe Ala Glu Ile
               2515   2520   2525

gca cgc agc gtg gac tac cgg cgt ggc gac cta ccg gtc gtg tcg acg   7632
Ala Arg Ser Val Asp Tyr Arg Arg Gly Asp Leu Pro Val Val Ser Thr
2530   2535   2540

ttg acg ggt gag ctc gac acc gca ggt gtg atg gct acg ccg gag tat   7680
Leu Thr Gly Glu Leu Asp Thr Ala Gly Val Met Ala Thr Pro Glu Tyr
2545   2550   2555   2560

tgg gtg cgt cag gtt cga gag ccc gtc cgc ttc gcc gac ggc gtc cgg   7728
Trp Val Arg Gln Val Arg Glu Pro Val Arg Phe Ala Asp Gly Val Arg
               2565   2570   2575

```
gtg ctc gcg cag caa ggg gtc gcc acg atc ttc gaa ctc ggc cct gat    7776
Val Leu Ala Gln Gln Gly Val Ala Thr Ile Phe Glu Leu Gly Pro Asp
         2580                2585                2590


gcg acg ctg tcg gcc ctg att ccc gat tgt cat tcg tgg gct gat cag    7824
Ala Thr Leu Ser Ala Leu Ile Pro Asp Cys His Ser Trp Ala Asp Gln
         2595                2600                2605


gcc atg ccg att ccg atg ctg cgt aaa gac cgt acg gaa acc gaa act    7872
Ala Met Pro Ile Pro Met Leu Arg Lys Asp Arg Thr Glu Thr Glu Thr
    2610                2615                2620


gtg gtc gcc gcg gtg gcg cgg gcg cac acg cgt ggt gtt ccg gtc gaa    7920
Val Val Ala Ala Val Ala Arg Ala His Thr Arg Gly Val Pro Val Glu
2625                2630                2635                2640


tgg tcg gcg tat ttc gcc ggc acc ggg gca cgg cgg gtc gag ttg ccg    7968
Trp Ser Ala Tyr Phe Ala Gly Thr Gly Ala Arg Arg Val Glu Leu Pro
             2645                2650                2655


acg tat gcc ttc cag cgg cag cgg tac tgg ctg gaa aca tcg gat tac    8016
Thr Tyr Ala Phe Gln Arg Gln Arg Tyr Trp Leu Glu Thr Ser Asp Tyr
         2660                2665                2670


ggc gat gtg acg ggt atc ggc ctg gct gcg gcg gag cat ccg ttg ctg    8064
Gly Asp Val Thr Gly Ile Gly Leu Ala Ala Ala Glu His Pro Leu Leu
         2675                2680                2685


ggg gcc gtg gtt gcg ctg gcc gat ggt gat ggg atg gtg ctg acc ggc    8112
Gly Ala Val Val Ala Leu Ala Asp Gly Asp Gly Met Val Leu Thr Gly
    2690                2695                2700


cgg ttg tcg gtg ggg acg cat ccg tgg ctg gcc cag cat cgc gtg ctg    8160
Arg Leu Ser Val Gly Thr His Pro Trp Leu Ala Gln His Arg Val Leu
2705                2710                2715                2720


ggc gag gtc gtc gtc ccc ggc acc gcc atc ctg gag atg gcc ctg cac    8208
Gly Glu Val Val Val Pro Gly Thr Ala Ile Leu Glu Met Ala Leu His
             2725                2730                2735


gca ggg gcg cgt ctc ggc tgt gac cgg gtg gaa gag ctc acc ctg gaa    8256
Ala Gly Ala Arg Leu Gly Cys Asp Arg Val Glu Glu Leu Thr Leu Glu
         2740                2745                2750


aca ccg ctg gtg gtc ccc gaa cgc gcg gcg ggt gcc ggt agt cgt ggc    8304
Thr Pro Leu Val Val Pro Glu Arg Ala Ala Gly Ala Gly Ser Arg Gly
         2755                2760                2765
```

285

```
cct gcg gga ggg acc aca gtt tca att gaa act gcg gaa gaa cgt gtg   8352
Pro Ala Gly Gly Thr Thr Val Ser Ile Glu Thr Ala Glu Glu Arg Val
    2770            2775            2780
```

```
cgg acg aac gac gcc atc gaa atc cag ctg ctg gtg aac gca ccc gac   8400
Arg Thr Asn Asp Ala Ile Glu Ile Gln Leu Leu Val Asn Ala Pro Asp
2785            2790            2795            2800
```

```
gaa ggc ggt cgg cga agg gtg tcg ctg tat tcc cgc ccg gcc ggt ggg   8448
Glu Gly Gly Arg Arg Arg Val Ser Leu Tyr Ser Arg Pro Ala Gly Gly
        2805            2810            2815
```

```
tcg aga ggt ggg ggt tgg acg cgc cac gcc acc ggc gaa ctc gtc gtc   8496
Ser Arg Gly Gly Gly Trp Thr Arg His Ala Thr Gly Glu Leu Val Val
        2820            2825            2830
```

```
ggc acc acc ggt ggt agg gcg gtt cct gat tgg tcg gct gag ggt gcc   8544
Gly Thr Thr Gly Gly Arg Ala Val Pro Asp Trp Ser Ala Glu Gly Ala
        2835            2840            2845
```

```
gag tcg att gct ctc gat gag ttc tac gtc gct ctg gcc gga aac ggg   8592
Glu Ser Ile Ala Leu Asp Glu Phe Tyr Val Ala Leu Ala Gly Asn Gly
        2850            2855            2860
```

```
ttc gag tac ggg ccg ttg ttc cag ggg ctt cag gcg gca tgg cgt cgt   8640
Phe Glu Tyr Gly Pro Leu Phe Gln Gly Leu Gln Ala Ala Trp Arg Arg
2865            2870            2875            2880
```

```
ggt gac gag gtt ctc gcc gaa atc gcc ccg ccg gcc gag gcc gat gcg   8688
Gly Asp Glu Val Leu Ala Glu Ile Ala Pro Pro Ala Glu Ala Asp Ala
            2885            2890            2895
```

```
atg gcg tcg gga tac ctg ctc gac cca gcg ttg ctg gat gcc gcg ctg   8736
Met Ala Ser Gly Tyr Leu Leu Asp Pro Ala Leu Leu Asp Ala Ala Leu
            2900            2905            2910
```

```
cag gcg tcc gcg ctc ggc gac cgc ccg gag caa ggc ggc gcg tgg ctg   8784
Gln Ala Ser Ala Leu Gly Asp Arg Pro Glu Gln Gly Gly Ala Trp Leu
        2915            2920            2925
```

```
ccg ttc tca ttc acc ggc gtc gaa ctt tcc gct ccg gca ggg acg atc   8832
Pro Phe Ser Phe Thr Gly Val Glu Leu Ser Ala Pro Ala Gly Thr Ile
    2930            2935            2940
```

```
agc agg gtg cgg ctg gag acc agg cga ccc gac gcg ata tcg gtg gcc   8880
Ser Arg Val Arg Leu Glu Thr Arg Arg Pro Asp Ala Ile Ser Val Ala
2945            2950            2955            2960
```

286

```
gtg atg gat gag agt ggg cgg ttg ctc gcc tcg atc gat tct ctc agg   8928
Val Met Asp Glu Ser Gly Arg Leu Leu Ala Ser Ile Asp Ser Leu Arg
            2965               2970               2975


cta cga agc gtg tcg tcg gga cag ctg gcg aat cgg gac gct gtc cgc   8976
Leu Arg Ser Val Ser Ser Gly Gln Leu Ala Asn Arg Asp Ala Val Arg
            2980               2985               2990


gac gcg ctg ttc gag gtg acc tgg gag ccg gtg gcg acg cag tcg acg   9024
Asp Ala Leu Phe Glu Val Thr Trp Glu Pro Val Ala Thr Gln Ser Thr
            2995               3000               3005


gaa ccg ggt cgc tgg gcc ctg ctt ggt gat act gcc tgc ggt aaa gac   9072
Glu Pro Gly Arg Trp Ala Leu Leu Gly Asp Thr Ala Cys Gly Lys Asp
      3010               3015               3020


gat ctc atc aaa ctc gca acg gat tcc gcc gac cgc tgc gcg gat ctg   9120
Asp Leu Ile Lys Leu Ala Thr Asp Ser Ala Asp Arg Cys Ala Asp Leu
3025               3030               3035               3040


gcg gcg cta gcc gag aaa ctt gat tcc agc gcg ctg gtt cct gat gtc   9168
Ala Ala Leu Ala Glu Lys Leu Asp Ser Ser Ala Leu Val Pro Asp Val
            3045               3050               3055


gtg gtc tac tgc gcc gga gaa cag gcg gat ccc ggc acc ggc gca gcc   9216
Val Val Tyr Cys Ala Gly Glu Gln Ala Asp Pro Gly Thr Gly Ala Ala
            3060               3065               3070


gca ctt gcg gag acc cag cag acg ttg gct ctg ctc caa gcg tgg ttg   9264
Ala Leu Ala Glu Thr Gln Gln Thr Leu Ala Leu Leu Gln Ala Trp Leu
         3075               3080               3085


gct gag ccg cgg ttg gcc gag gca cgt ctg gtg gtg gtg acg tgt gca   9312
Ala Glu Pro Arg Leu Ala Glu Ala Arg Leu Val Val Val Thr Cys Ala
         3090               3095               3100


gcg gtg acg acg gct ccg agt gac ggt gca tca gag ctg gca cat gcg   9360
Ala Val Thr Thr Ala Pro Ser Asp Gly Ala Ser Glu Leu Ala His Ala
3105               3110               3115               3120


ccg ttg tgg ggg ttg ttg cgt gcc gcg cag gtg gag aac ccg ggg cag   9408
Pro Leu Trp Gly Leu Leu Arg Ala Ala Gln Val Glu Asn Pro Gly Gln
            3125               3130               3135


ttt gtg ctg gcg gac gtc gac gga acc gcc gaa tcg tgg cgt gcg ttg   9456
Phe Val Leu Ala Asp Val Asp Gly Thr Ala Glu Ser Trp Arg Ala Leu
            3140               3145               3150
```

287

```
ccg agt gcg ttg ggc tcg atg gaa ccg cag ttg gcc ctg cgg aag ggc      9504
Pro Ser Ala Leu Gly Ser Met Glu Pro Gln Leu Ala Leu Arg Lys Gly
        3155            3160            3165


gcg gtg cga gcg ccc cgc ttg gct tcg gtc gcc ggg cag atc gac gtg      9552
Ala Val Arg Ala Pro Arg Leu Ala Ser Val Ala Gly Gln Ile Asp Val
    3170            3175            3180


ccc gcg gtt gtg gcg gat ccc gac cga acc gtg ctg att tcg ggc ggc      9600
Pro Ala Val Val Ala Asp Pro Asp Arg Thr Val Leu Ile Ser Gly Gly
3185            3190             3195            3200


acg ggc ctg ttg ggg ggc gcg gtt gcc cgc cac ctg gtg acc gaa cgc      9648
Thr Gly Leu Leu Gly Gly Ala Val Ala Arg His Leu Val Thr Glu Arg
            3205            3210            3215


ggt gtc cgc cga ttg gtg ttg acg ggc cgt cgt ggc tgg gat gct cct      9696
Gly Val Arg Arg Leu Val Leu Thr Gly Arg Arg Gly Trp Asp Ala Pro
            3220            3225            3230


gga atc acc gag ttg gtg ggt gag ctg aac ggc ctc ggt gcc gtg gtc      9744
Gly Ile Thr Glu Leu Val Gly Glu Leu Asn Gly Leu Gly Ala Val Val
        3235            3240            3245


gac gtg gtg gcg tgc gac gtc gcg gat cgt gct gat ctg gag tcg ttg      9792
Asp Val Val Ala Cys Asp Val Ala Asp Arg Ala Asp Leu Glu Ser Leu
    3250            3255            3260


ctg gcg gcg gtc ccg gcg gaa ttt ccg ttg tgc ggc gtg gtg cat gcc      9840
Leu Ala Ala Val Pro Ala Glu Phe Pro Leu Cys Gly Val Val His Ala
3265            3270            3275            3280


gcg ggg gcg ctg gcc gac ggg gtg atc gag tcg ttg tca ccg gac gac      9888
Ala Gly Ala Leu Ala Asp Gly Val Ile Glu Ser Leu Ser Pro Asp Asp
            3285            3290            3295


gtg gga gcg gtg ttc ggc ccg aag gcg gcg ggg gcg tgg aat ctg cac      9936
Val Gly Ala Val Phe Gly Pro Lys Ala Ala Gly Ala Trp Asn Leu His
            3300            3305            3310


gag ctg act cgt gat acg gac ctg tcg ttc ttc gcg ttg ttc tcc tcg      9984
Glu Leu Thr Arg Asp Thr Asp Leu Ser Phe Phe Ala Leu Phe Ser Ser
        3315            3320            3325


ctt tcc ggt gtt gcc ggc gct cct ggt cag ggc aat tat gcg gcg gcg     10032
Leu Ser Gly Val Ala Gly Ala Pro Gly Gln Gly Asn Tyr Ala Ala Ala
        3330            3335            3340
```

288

```
aac gcg ttc ctg gac gca ttg gcg cat tac cgg cgg tca cag gga ctg     10080
Asn Ala Phe Leu Asp Ala Leu Ala His Tyr Arg Arg Ser Gln Gly Leu
3345              3350              3355              3360


cct gcg gtg tcg ctg gcc tgg ggc ctg tgg gag cag ccg agc ggg atg     10128
Pro Ala Val Ser Leu Ala Trp Gly Leu Trp Glu Gln Pro Ser Gly Met
              3365              3370              3375


acg gag acg ctc agc gag gtc gac cgg agc agg atc gcg cgc gcc aac     10176
Thr Glu Thr Leu Ser Glu Val Asp Arg Ser Arg Ile Ala Arg Ala Asn
              3380              3385              3390


ccg ccg ttg tcc acc aag gag gga ttg cgg ctg ttc gat gcc ggg ctg     10224
Pro Pro Leu Ser Thr Lys Glu Gly Leu Arg Leu Phe Asp Ala Gly Leu
              3395              3400              3405


gcg ctg gac cgg gca gcg gta gtt ccg gcg aag ttg gac agg act ttc     10272
Ala Leu Asp Arg Ala Ala Val Val Pro Ala Lys Leu Asp Arg Thr Phe
3410              3415              3420


ctg gcc gag cag gcg cgg tcg ggc tcg ctg ccc gca ttg ttg acg gca     10320
Leu Ala Glu Gln Ala Arg Ser Gly Ser Leu Pro Ala Leu Leu Thr Ala
3425              3430              3435              3440


ctg gta ccc ccc atc cgt cgt aat agg cgg gct agc gga acc gag ctc     10368
Leu Val Pro Pro Ile Arg Arg Asn Arg Arg Ala Ser Gly Thr Glu Leu
              3445              3450              3455


gcg gac gag ggc acc ctg ctc ggg gtg gtg cgg gag cat gcc gcg gcc     10416
Ala Asp Glu Gly Thr Leu Leu Gly Val Val Arg Glu His Ala Ala Ala
              3460              3465              3470


gtg ctg ggg tat tcg agc gcg gct gac gtc ggg gtc gag cgc gct ttc     10464
Val Leu Gly Tyr Ser Ser Ala Ala Asp Val Gly Val Glu Arg Ala Phe
              3475              3480              3485


cgg gat ctg ggt ttt gat tcg ttg tct ggt gtg gag ttg cgg aac cgc     10512
Arg Asp Leu Gly Phe Asp Ser Leu Ser Gly Val Glu Leu Arg Asn Arg
              3490              3495              3500


ctt gcc ggg gtg ctg ggg gtg cgg ttg ccg gcg act gcg gtg ttc gac     10560
Leu Ala Gly Val Leu Gly Val Arg Leu Pro Ala Thr Ala Val Phe Asp
3505              3510              3515              3520


tat ccg acg ccg agg gcg ctg gcc cgg ttc ctg cac cag gaa ctg gca     10608
Tyr Pro Thr Pro Arg Ala Leu Ala Arg Phe Leu His Gln Glu Leu Ala
              3525              3530              3535
```

289

```
gac gag atc gct acg acg cca gcg ccg gtg acg acg acc agg gca ccg        10656
Asp Glu Ile Ala Thr Thr Pro Ala Pro Val Thr Thr Thr Arg Ala Pro          .
        3540            3545                3550


gtc gcc gaa gac gat ctc gtc gcg ata gtc ggg atg gga tgc cgt ttt        10704
Val Ala Glu Asp Asp Leu Val Ala Ile Val Gly Met Gly Cys Arg Phe
        3555            3560                3565


ccc ggt cag gtg tcc tcg ccg gag gag ctc tgg cgt ttg gtg gcc ggg        10752
Pro Gly Gln Val Ser Ser Pro Glu Glu Leu Trp Arg Leu Val Ala Gly
    3570            3575            3580


ggc gtg gat gcg gtc gcg gac ttc cca gcc gat cgc ggc tgg gat ctg        10800
Gly Val Asp Ala Val Ala Asp Phe Pro Ala Asp Arg Gly Trp Asp Leu
3585            3590            3595            3600


gca ggc ttg ttc gat ccg gac ccg gaa cgg gct ggg aag acc tac gtg        10848
Ala Gly Leu Phe Asp Pro Asp Pro Glu Arg Ala Gly Lys Thr Tyr Val
            3605            3610            3615


cgg gaa ggg gcc ttc ctc acc gac gcc gat cgg ttc gat gcg ggt ttc        10896
Arg Glu Gly Ala Phe Leu Thr Asp Ala Asp Arg Phe Asp Ala Gly Phe
        3620            3625            3630


ttc ggg att tcc ccg cgt gag gcg ttg gcg atg gat ccg cag caa cgg        10944
Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg
        3635            3640            3645


ctg ttg ctg gag ctg tcc tgg gag gcc att gaa cgg gca ggg atc gat        10992
Leu Leu Leu Glu Leu Ser Trp Glu Ala Ile Glu Arg Ala Gly Ile Asp
    3650            3655            3660


ccg ggt tcg ctg agg ggg agt cgg acc ggt gtg ttc gcg ggg ctg atg        11040
Pro Gly Ser Leu Arg Gly Ser Arg Thr Gly Val Phe Ala Gly Leu Met
3665            3670            3675            3680


tac cac gac tat ggc gcc cgg ttc gcc agc cga gcc ccg gaa ggt ttc        11088
Tyr His Asp Tyr Gly Ala Arg Phe Ala Ser Arg Ala Pro Glu Gly Phe
            3685            3690            3695


gag ggg tat ctc ggc aat ggc agt gct ggg agt gtc gcg tcg ggc cgg        11136
Glu Gly Tyr Leu Gly Asn Gly Ser Ala Gly Ser Val Ala Ser Gly Arg
            3700            3705            3710


att gcg tac tcg ttt ggt ttc gag ggt cct gcg gtg acg gtg gat act        11184
Ile Ala Tyr Ser Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr
        3715            3720            3725
```

290

gcg tgt tcg tcg tcg ttg gtg gcg ttg cat ttg gcg ggt cag tcg ttg   11232
Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala Gly Gln Ser Leu
    3730   3735   3740

cgt tcc ggc gaa tgc gat ctc gcc ctt gcc ggt ggt gtg acg gtg atg   11280
Arg Ser Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met
3745   3750   3755   3760

tcg acg ccc ggg acg ttt gtg gaa ttc tcc cgt cag cgg ggc ctg gca   11328
Ser Thr Pro Gly Thr Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala
            3765   3770   3775

ccg gac ggg cgg tgc aag tcg ttc gcg gag agc gcg gac ggt acc ggt   11376
Pro Asp Gly Arg Cys Lys Ser Phe Ala Glu Ser Ala Asp Gly Thr Gly
            3780   3785   3790

tgg ggt gag ggt gct ggt ttg gtg ttg ttg gag cgg ttg tcg gat gct   11424
Trp Gly Glu Gly Ala Gly Leu Val Leu Leu Glu Arg Leu Ser Asp Ala
    3795   3800   3805

cgg cgg aat ggg cat cgg gtg ttg gcg gtg gtt cgt ggg tcg gcg gtg   11472
Arg Arg Asn Gly His Arg Val Leu Ala Val Val Arg Gly Ser Ala Val
    3810   3815   3820

aat cag gat ggt gcg tcg aat ggc ttg acc gcg ccg aat ggt ccc tcg   11520
Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser
3825   3830   3835   3840

cag cag cgg gtc atc cag cag gcg ttg gcg agt gcg ggt ctg tcg gtg   11568
Gln Gln Arg Val Ile Gln Gln Ala Leu Ala Ser Ala Gly Leu Ser Val
            3845   3850   3855

tcc gat gtg gat gcc gtg gag gcg cat ggg acc ggg acc agg ttg ggt   11616
Ser Asp Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly
            3860   3865   3870

gat ccg att gag gcg cag gct ctg att gct acg tat ggg cgc gat cgt   11664
Asp Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr Tyr Gly Arg Asp Arg
        3875   3880   3885

gat ccc ggt cgg ccg ttg tgg ttg ggg tcg gtg aag tcc aac atc ggt   11712
Asp Pro Gly Arg Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile Gly
    3890   3895   3900

cat acg cag gcg gcg gcg ggt gtt gcc ggt gtg atc aag atg gtg atg   11760
His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Met
3905   3910   3915   3920

291

```
gcg atg cgg cac ggg caa ctt ccg cgc acg ctg cac gtg gat gca ccc    11808
Ala Met Arg His Gly Gln Leu Pro Arg Thr Leu His Val Asp Ala Pro
        3925                3930                3935


tcc tcg cag gtg gat tgg tcg gcg ggg agg gtc cag ctc ctg acg gag    11856
Ser Ser Gln Val Asp Trp Ser Ala Gly Arg Val Gln Leu Leu Thr Glu
        3940                3945                3950


aac acg ccc tgg ccc gac agt ggt cgc ccc tgt cgg gtg ggg gtg tcg    11904
Asn Thr Pro Trp Pro Asp Ser Gly Arg Pro Cys Arg Val Gly Val Ser
        3955                3960                3965


tcg ttc ggg atc agc ggc acc aac gcg cac gtc atc ctg gaa cag tcc    11952
Ser Phe Gly Ile Ser Gly Thr Asn Ala His Val Ile Leu Glu Gln Ser
       3970                3975                3980


acg ggg cag atg gat cag gca gcg gag ccg gat tcg agt cct gtt ctg    12000
Thr Gly Gln Met Asp Gln Ala Ala Glu Pro Asp Ser Ser Pro Val Leu
3985                3990                3995                4000


gat gtt ccg gtg gtg ccg tgg gtg gtg tcg ggc aaa aca ccc gaa gcg    12048
Asp Val Pro Val Val Pro Trp Val Val Ser Gly Lys Thr Pro Glu Ala
                4005                4010                4015


cta tcc gcc cag gcg gca acg ttg gcg acc tat ttg gac caa aat gtt    12096
Leu Ser Ala Gln Ala Ala Thr Leu Ala Thr Tyr Leu Asp Gln Asn Val
               4020                4025                4030


gat gtc tcc cct ctg gac gtt ggg att tcg ctt gcg gtg acc cgt tcg    12144
Asp Val Ser Pro Leu Asp Val Gly Ile Ser Leu Ala Val Thr Arg Ser
       4035                4040                4045


gcg ctg gat gag cgg gcg gtg gtg ctg ggg tcg gat cgt gac acg ttg    12192
Ala Leu Asp Glu Arg Ala Val Val Leu Gly Ser Asp Arg Asp Thr Leu
   4050                4055                4060


ttg tct ggc ctg aat gcg ctg gct gcc ggt cat gag gct gct ggc gtg    12240
Leu Ser Gly Leu Asn Ala Leu Ala Ala Gly His Glu Ala Ala Gly Val
4065                4070                4075                4080


gtt acg gga cct gtc ggg att ggt ggc cgg acc ggg ttt gtg ttc gcc    12288
Val Thr Gly Pro Val Gly Ile Gly Gly Arg Thr Gly Phe Val Phe Ala
                4085                4090                4095


ggt caa ggc ggt cag tgg ttg ggg atg ggc cgc cgg ttg tac tcg gag    12336
Gly Gln Gly Gly Gln Trp Leu Gly Met Gly Arg Arg Leu Tyr Ser Glu
                4100                4105                4110
```

ttt ccg gcg ttc gcc ggt gct ttc gac gaa gca tgc gcc gag ctc gat   12384
Phe Pro Ala Phe Ala Gly Ala Phe Asp Glu Ala Cys Ala Glu Leu Asp
        4115   4120   4125

gcg aac ctg ggg agg gaa gtc ggg gtt cgg gat gtg gtg ttc ggc tcc   12432
Ala Asn Leu Gly Arg Glu Val Gly Val Arg Asp Val Val Phe Gly Ser
        4130   4135   4140

gac gag tcc ttg ctg gat cgg act ttg tgg gcg cag tcg ggt ttg ttc   12480
Asp Glu Ser Leu Leu Asp Arg Thr Leu Trp Ala Gln Ser Gly Leu Phe
4145   4150   4155   4160

gcg ttg cag gtc ggt ctc tgg gaa ttg ttg ggt acg tgg ggt gtt cgg   12528
Ala Leu Gln Val Gly Leu Trp Glu Leu Leu Gly Thr Trp Gly Val Arg
            4165   4170   4175

ccc agc gta gtg ctg ggg cat tcg gtc ggg gag cta gcc gcg gcg ttc   12576
Pro Ser Val Val Leu Gly His Ser Val Gly Glu Leu Ala Ala Ala Phe
            4180   4185   4190

gcc gca ggt gtg ctg tcg atg gcg gag gcg gct cgg ctg gtg gcg ggt   12624
Ala Ala Gly Val Leu Ser Met Ala Glu Ala Ala Arg Leu Val Ala Gly
        4195   4200   4205

cgt gcg cgg ttg atg cag gcg ttg cct tct ggc ggt gcc atg ctg gcg   12672
Arg Ala Arg Leu Met Gln Ala Leu Pro Ser Gly Gly Ala Met Leu Ala
        4210   4215   4220

gtg tcc gcg acc gag gcc cga gtc ggc ccg ctg ctc gat ggg gtg cgg   12720
Val Ser Ala Thr Glu Ala Arg Val Gly Pro Leu Leu Asp Gly Val Arg
4225   4230   4235   4240

gat cgt gtt ggt gtc gca gcg gtt aac gct ccg ggg tcg gtg gtg ctt   12768
Asp Arg Val Gly Val Ala Ala Val Asn Ala Pro Gly Ser Val Val Leu
            4245   4250   4255

tcc ggt gac cgg gat gtg ctc gat ggc att gcc ggt cgg ctg gac ggg   12816
Ser Gly Asp Arg Asp Val Leu Asp Gly Ile Ala Gly Arg Leu Asp Gly
            4260   4265   4270

caa ggt atc cgg tcg agg tgg ttg cgg gtt tcg cac gcg ttt cat tcg   12864
Gln Gly Ile Arg Ser Arg Trp Leu Arg Val Ser His Ala Phe His Ser
        4275   4280   4285

cat cgg atg gat ccg atg ctg gcg gag ttc gcc gag ctc gca cgg agc   12912
His Arg Met Asp Pro Met Leu Ala Glu Phe Ala Glu Leu Ala Arg Ser
        4290   4295   4300

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gtg gac tac cgg tct cca cgg ctg ccg att gtc tcg acg ctg acc gga    12960
Val Asp Tyr Arg Ser Pro Arg Leu Pro Ile Val Ser Thr Leu Thr Gly
4305              4310              4315              4320

aac ctc gat gac gtg ggc gtg atg gct acg ccg gag tat tgg gtg cgc    13008
Asn Leu Asp Asp Val Gly Val Met Ala Thr Pro Glu Tyr Trp Val Arg
             4325              4330              4335

cag gtg cga gag ccc gtc cgc ttc gcc gac ggt gtc cag gcg ctt gtg    13056
Gln Val Arg Glu Pro Val Arg Phe Ala Asp Gly Val Gln Ala Leu Val
         4340              4345              4350

gac caa ggc gtc gac acg att gtg gaa ctc ggt ccg gac ggg gcg ttg    13104
Asp Gln Gly Val Asp Thr Ile Val Glu Leu Gly Pro Asp Gly Ala Leu
         4355              4360              4365

tcg agc ttg gtt caa gag tgt gtg gcg gag tcc ggg cgg gcg acg ggg    13152
Ser Ser Leu Val Gln Glu Cys Val Ala Glu Ser Gly Arg Ala Thr Gly
     4370              4375              4380

att ccg ttg gtg cgg aga gac cgt gat gag gtc cga acg gtg ctg gac    13200
Ile Pro Leu Val Arg Arg Asp Arg Asp Glu Val Arg Thr Val Leu Asp
4385              4390              4395              4400

gct ttg gcg cag acc cac act cgt ggt ggc gcg gtg gac tgg ggg tca    13248
Ala Leu Ala Gln Thr His Thr Arg Gly Gly Ala Val Asp Trp Gly Ser
             4405              4410              4415

ttt ttc gct ggt acg agg gca acg caa gtc gac ctt ccc acg tat gcc    13296
Phe Phe Ala Gly Thr Arg Ala Thr Gln Val Asp Leu Pro Thr Tyr Ala
         4420              4425              4430

ttc caa cga cag cgg tac tgg ctg gag cca tcg gat tcc ggt gat gtg    13344
Phe Gln Arg Gln Arg Tyr Trp Leu Glu Pro Ser Asp Ser Gly Asp Val
         4435              4440              4445

acc ggt gtt ggc ctg acc ggg gcg gag cat ccg ctg ttg ggt gcc gtg    13392
Thr Gly Val Gly Leu Thr Gly Ala Glu His Pro Leu Leu Gly Ala Val
     4450              4455              4460

gtg ccg gtc gcg ggc ggc gat gag gtg ctg ctg acc ggc agg ctg tcg    13440
Val Pro Val Ala Gly Gly Asp Glu Val Leu Leu Thr Gly Arg Leu Ser
4465              4470              4475              4480

gtg ggg acg cat ccg tgg ctg gcg gaa cac cgc gtg ctg ggc gaa gtc    13488
Val Gly Thr His Pro Trp Leu Ala Glu His Arg Val Leu Gly Glu Val
             4485              4490              4495
```

```
gtc gtc ccc ggc acc gcg ttg ctg gag atg gcg tgg cgg gcc ggt agc      13536
Val Val Pro Gly Thr Ala Leu Leu Glu Met Ala Trp Arg Ala Gly Ser
            4500                4505                4510


cag gtc ggt tgt gaa cgt gtg gag gag ctc acc ttg gag gca ccg ctg      13584
Gln Val Gly Cys Glu Arg Val Glu Glu Leu Thr Leu Glu Ala Pro Leu
        4515                4520                4525


gtc ctg ccg gag cgg ggc gct gcg gcg gtg cag ttg gcg gtg ggg gct      13632
Val Leu Pro Glu Arg Gly Ala Ala Ala Val Gln Leu Ala Val Gly Ala
        4530                4535                4540


ccg gat gag gcc ggc cgg cgc agt ttg cag ctc tat tcc cga ggc gct      13680
Pro Asp Glu Ala Gly Arg Arg Ser Leu Gln Leu Tyr Ser Arg Gly Ala
4545                4550                4555                4560


gat gaa gac ggc gac tgg cgg cgg att gcc tcc ggg ctg ttg gcc cag      13728
Asp Glu Asp Gly Asp Trp Arg Arg Ile Ala Ser Gly Leu Leu Ala Gln
            4565                4570                4575


gcc aat gcg gtg ccg ccg gcg gat tcg acg gca tgg ccg ccg gac ggc      13776
Ala Asn Ala Val Pro Pro Ala Asp Ser Thr Ala Trp Pro Pro Asp Gly
                4580                4585                4590


gcc ggg cag gtc gat ctg gcg gag ttc tac gag cgc ctc gcc gag cgc      13824
Ala Gly Gln Val Asp Leu Ala Glu Phe Tyr Glu Arg Leu Ala Glu Arg
            4595                4600                4605


ggc ttg acc tac ggt ccg gta ttc caa ggg ctc cgc gcc gca tgg cgg      13872
Gly Leu Thr Tyr Gly Pro Val Phe Gln Gly Leu Arg Ala Ala Trp Arg
        4610                4615                4620


cac ggc gac gat atc ttc gcc gaa ttg gcc ggg tca cca gac gcc tcg      13920
His Gly Asp Asp Ile Phe Ala Glu Leu Ala Gly Ser Pro Asp Ala Ser
4625                4630                4635                4640


ggt ttc ggc atc cac ccg gcg ctg ctg gac gct gca ctg cac gcg atg      13968
Gly Phe Gly Ile His Pro Ala Leu Leu Asp Ala Ala Leu His Ala Met
                4645                4650                4655


gcg ctt ggt gct tcg ccc gac tcg gaa gcg cgt ctg ccg ttt tcc tgg      14016
Ala Leu Gly Ala Ser Pro Asp Ser Glu Ala Arg Leu Pro Phe Ser Trp
            4660                4665                4670


cgt ggc gcc cag ctg tac cgc gct gaa gga gca gcg ctt cgg gta cgg      14064
Arg Gly Ala Gln Leu Tyr Arg Ala Glu Gly Ala Ala Leu Arg Val Arg
        4675                4680                4685
```

ctc tcg ccg ctg ggc tcc ggt gca gtc tca ttg acg ttg gtg gat gcc   14112
Leu Ser Pro Leu Gly Ser Gly Ala Val Ser Leu Thr Leu Val Asp Ala
    4690   4695   4700

aca ggg cga cga gtc gct gcg gtg gaa tcg ctt tcg acg cga ccg gtc   14160
Thr Gly Arg Arg Val Ala Ala Val Glu Ser Leu Ser Thr Arg Pro Val
4705   4710   4715   4720

tcc acc gac cag atc ggt gcc ggt cgc ggc gat caa gag cgg ctg ctg   14208
Ser Thr Asp Gln Ile Gly Ala Gly Arg Gly Asp Gln Glu Arg Leu Leu
          4725   4730   4735

cac gtc gag tgg gta agg tcg gct gaa tct gcg ggg atg tct ctg acc   14256
His Val Glu Trp Val Arg Ser Ala Glu Ser Ala Gly Met Ser Leu Thr
          4740   4745   4750

tcc tgc gcg gtg gtc ggt ttg ggc gaa ccg gag tgg cac gct gcg ctg   14304
Ser Cys Ala Val Val Gly Leu Gly Glu Pro Glu Trp His Ala Ala Leu
          4755   4760   4765

aag acc act ggt gtc caa gtc gag tcc cat gcg gac ctt gct tcg ttg   14352
Lys Thr Thr Gly Val Gln Val Glu Ser His Ala Asp Leu Ala Ser Leu
          4770   4775   4780

gcc acc gag gtt gcc aag cgg ggt tca gct cct ggt gcg gtc atc gtc   14400
Ala Thr Glu Val Ala Lys Arg Gly Ser Ala Pro Gly Ala Val Ile Val
4785   4790   4795   4800

ccg tgc ccg cga ccc cga gcg atg cag gag ctg ccg acc gcc gcg cga   14448
Pro Cys Pro Arg Pro Arg Ala Met Gln Glu Leu Pro Thr Ala Ala Arg
              4805   4810   4815

agg gcg acg caa cag gcg atg gcg atg ctg cag caa tgg ctt gcc gat   14496
Arg Ala Thr Gln Gln Ala Met Ala Met Leu Gln Gln Trp Leu Ala Asp
              4820   4825   4830

gac cgg ttc gtc agt acg cgc ctg atc ctg ctg acg cat cgg gcg gtc   14544
Asp Arg Phe Val Ser Thr Arg Leu Ile Leu Leu Thr His Arg Ala Val
          4835   4840   4845

tcc gca gtt gct gga gaa gac gtg ctc gac ctg gta cac gcg ccg ctg   14592
Ser Ala Val Ala Gly Glu Asp Val Leu Asp Leu Val His Ala Pro Leu
          4850   4855   4860

tgg ggc ttg gtc cgc agc gcg caa gcg gag cac ccg gac cga ttc gcc   14640
Trp Gly Leu Val Arg Ser Ala Gln Ala Glu His Pro Asp Arg Phe Ala
4865   4870   4875   4880

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ttg atc gat atg gac gac gag cga gca tcg cag acg gca ctc gcc gaa     14688
Leu Ile Asp Met Asp Asp Glu Arg Ala Ser Gln Thr Ala Leu Ala Glu
            4885            4890            4895

gcg ctg act gcg gga gaa gcg cag ctc gcg gtg cgg tcg gga gtt gtg     14736
Ala Leu Thr Ala Gly Glu Ala Gln Leu Ala Val Arg Ser Gly Val Val
            4900            4905            4910

ctg gcg ccc cgc ctc ggc cag gtg aag gtg agt gga ggt gaa gcg ttc     14784
Leu Ala Pro Arg Leu Gly Gln Val Lys Val Ser Gly Gly Glu Ala Phe
        4915            4920            4925

agg tgg gat gaa ggc acc gtg ctg gtc acc ggc gga acc ggc ggg ctc     14832
Arg Trp Asp Glu Gly Thr Val Leu Val Thr Gly Gly Thr Gly Gly Leu
        4930            4935            4940

ggg gcc ctg ctc gca cgc cat ctg gtc agc gcc cac ggt gtg cgg cac     14880
Gly Ala Leu Leu Ala Arg His Leu Val Ser Ala His Gly Val Arg His
4945            4950            4955            4960

ctg ttg ctc gca agt cgc cgt ggt ctg gcg gcg ccc gga gcg gat gag     14928
Leu Leu Leu Ala Ser Arg Arg Gly Leu Ala Ala Pro Gly Ala Asp Glu
            4965            4970            4975

ctg gtg gcc gag ctg gag cag gcc ggc gcc gac gtc gcg gtc gtc gcg     14976
Leu Val Ala Glu Leu Glu Gln Ala Gly Ala Asp Val Ala Val Val Ala
            4980            4985            4990

tgc gac tcg gca gat cgg gac tcg ctt gcg cgg ctg gtg gcg tcg gtg     15024
Cys Asp Ser Ala Asp Arg Asp Ser Leu Ala Arg Leu Val Ala Ser Val
            4995            5000            5005

cct gcg gaa aac ccg ttg cgg gtg gtg gtg cac gcc gcc ggt gtg ctg     15072
Pro Ala Glu Asn Pro Leu Arg Val Val Val His Ala Ala Gly Val Leu
        5010            5015            5020

gat gac ggt gtg ctg atg tcg atg tcg ccg gag cgc ttg gac gcg gtg     15120
Asp Asp Gly Val Leu Met Ser Met Ser Pro Glu Arg Leu Asp Ala Val
5025            5030            5035            5040

ttg cgg ccc aaa gtg gat gcc gcg tgg tac ctg cac gag ctg act cgg     15168
Leu Arg Pro Lys Val Asp Ala Ala Trp Tyr Leu His Glu Leu Thr Arg
            5045            5050            5055

gaa ctc ggt ctg tcg gcg ttc gtg ttg ttc tcc tcg gtc gcg ggc ctg     15216
Glu Leu Gly Leu Ser Ala Phe Val Leu Phe Ser Ser Val Ala Gly Leu
        5060            5065            5070
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297

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ttc ggc ggt gcg ggg cag agc aat tac gct gcc ggc aac gct ttc ctg   15264
Phe Gly Gly Ala Gly Gln Ser Asn Tyr Ala Ala Gly Asn Ala Phe Leu
    5075                5080                5085

gat gcc ttg gcg cat tgc cgg cag gcc cag ggg ctg ccc gcg ctg tcg   15312
Asp Ala Leu Ala His Cys Arg Gln Ala Gln Gly Leu Pro Ala Leu Ser
    5090                5095                5100

ctg gcc tcc ggg ctg tgg gcg agt atc gat gga atg gcg ggc gac ctc   15360
Leu Ala Ser Gly Leu Trp Ala Ser Ile Asp Gly Met Ala Gly Asp Leu
5105                5110                5115                5120

gct gcg gca gat gtg gag cgg ctg tcg cgg gca ggc att ggc ccg ctt   15408
Ala Ala Ala Asp Val Glu Arg Leu Ser Arg Ala Gly Ile Gly Pro Leu
            5125                5130                5135

tcg gca ccg gga ggg ctg gcc ttg ttc gac gct gcc gtt ggc tcg gac   15456
Ser Ala Pro Gly Gly Leu Ala Leu Phe Asp Ala Ala Val Gly Ser Asp
            5140                5145                5150

gaa ccg ttg ctg gca ccg gtg cga ctg gat gtc gaa gca ctg cgt gtg   15504
Glu Pro Leu Leu Ala Pro Val Arg Leu Asp Val Glu Ala Leu Arg Val
            5155                5160                5165

cag gcc cga tcc gtg cag acc cgg att ccg gaa atg ctg cat ggc atg   15552
Gln Ala Arg Ser Val Gln Thr Arg Ile Pro Glu Met Leu His Gly Met
    5170                5175                5180

gca atg ggg cca agc cgc cgc act ccg ttc act tcc agg gtt gag ccg   15600
Ala Met Gly Pro Ser Arg Arg Thr Pro Phe Thr Ser Arg Val Glu Pro
5185                5190                5195                5200

ttg cac gaa cgg ctg gcc gga ttg tcg gag ggc gaa cgt cgg cag caa   15648
Leu His Glu Arg Leu Ala Gly Leu Ser Glu Gly Glu Arg Arg Gln Gln
            5205                5210                5215

gtg ctc cag cgc gtc cgc gcc gat atc gcg gtg gta ctg ggg cac ggc   15696
Val Leu Gln Arg Val Arg Ala Asp Ile Ala Val Val Leu Gly His Gly
            5220                5225                5230

agg tcg agc gat gtg gac atc gag aag cct ttg gcc gag ctg ggt ttc   15744
Arg Ser Ser Asp Val Asp Ile Glu Lys Pro Leu Ala Glu Leu Gly Phe
    5235                5240                5245

gac tcg ctg acg gcc atc gaa ctc cgc aac cgt ctc gct acc gcc acc   15792
Asp Ser Leu Thr Ala Ile Glu Leu Arg Asn Arg Leu Ala Thr Ala Thr
    5250                5255                5260
```

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gga ctg cgg ctt ccc gcg acg ctg gcc ttc gac cac ggc act gcg gcg    15840
Gly Leu Arg Leu Pro Ala Thr Leu Ala Phe Asp His Gly Thr Ala Ala
5265             5270             5275             5280

gca ctc gcc cag cac gtg tgc gcg cag cta ggc acc gcg acc gcg ccg    15888
Ala Leu Ala Gln His Val Cys Ala Gln Leu Gly Thr Ala Thr Ala Pro
             5285             5290             5295

gca ccg agg cga acc gac gac aac gac gcc acg gag ccc gtg agg tcg    15936
Ala Pro Arg Arg Thr Asp Asp Asn Asp Ala Thr Glu Pro Val Arg Ser
         5300             5305             5310

ctc ttc caa cag gcg tat gcg gct ggc cgg ata ctt gac ggg atg gat    15984
Leu Phe Gln Gln Ala Tyr Ala Ala Gly Arg Ile Leu Asp Gly Met Asp
         5315             5320             5325

ttg gtg aag gtc gct gcc cag ttg cga ccg gtg ttc ggt tcg cct ggc    16032
Leu Val Lys Val Ala Ala Gln Leu Arg Pro Val Phe Gly Ser Pro Gly
    5330             5335             5340

gag ctg gaa tcc ctg ccg aaa ccc gtc cag ctt tcc cgt ggt ccc gaa    16080
Glu Leu Glu Ser Leu Pro Lys Pro Val Gln Leu Ser Arg Gly Pro Glu
5345             5350             5355             5360

gag ctt gcc ttg gtg tgc atg ccg gcg ctg atc ggg atg ccg ccc gca    16128
Glu Leu Ala Leu Val Cys Met Pro Ala Leu Ile Gly Met Pro Pro Ala
             5365             5370             5375

cag cag tac gcg cgg atc gcc gcc ggg ttc cgc gat gtg cgg gac gtt    16176
Gln Gln Tyr Ala Arg Ile Ala Ala Gly Phe Arg Asp Val Arg Asp Val
         5380             5385             5390

tcg gtg atc ccg atg cct gga ttc att gcg gga gaa ccg ctg ccg tcc    16224
Ser Val Ile Pro Met Pro Gly Phe Ile Ala Gly Glu Pro Leu Pro Ser
    5395             5400             5405

gcc atc gag gtg gcg gtt cgg acg cag gcg gag gcg gtg ctg cag gaa    16272
Ala Ile Glu Val Ala Val Arg Thr Gln Ala Glu Ala Val Leu Gln Glu
    5410             5415             5420

ttc gcc ggg ggc tcg ttc gta ctg gtc ggg cat tcc tcc ggg ggc tgg    16320
Phe Ala Gly Gly Ser Phe Val Leu Val Gly His Ser Ser Gly Gly Trp
5425             5430             5435             5440

ctg gcg cac gag gta gcc ggt gag ctg gag cgt cgc ggg gtc gtc ccg    16368
Leu Ala His Glu Val Ala Gly Glu Leu Glu Arg Arg Gly Val Val Pro
             5445             5450             5455
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```
gcc ggg gtc gta ctg ctg gac acc tac atc ccc ggt gag atc acg ccg    16416
Ala Gly Val Val Leu Leu Asp Thr Tyr Ile Pro Gly Glu Ile Thr Pro
         5460                    5465                5470

agg ttc tcc gtg gcg atg gcc cac cgg acg tat gag aag ctc gcg act    16464
Arg Phe Ser Val Ala Met Ala His Arg Thr Tyr Glu Lys Leu Ala Thr
         5475                    5480                5485

ttc acg gac atg cag gat gtc ggt atc acc gcg atg ggc ggg tac ttc    16512
Phe Thr Asp Met Gln Asp Val Gly Ile Thr Ala Met Gly Gly Tyr Phe
     5490                5495                    5500

cgg atg ttc acc gag tgg act ccg acg ccg atc ggt gct ccg acg ctg    16560
Arg Met Phe Thr Glu Trp Thr Pro Thr Pro Ile Gly Ala Pro Thr Leu
5505            5510                5515                5520

ttc gtg cgg acc gaa gat tgc gtc gca gac cct gaa ggg cgg ccg tgg    16608
Phe Val Arg Thr Glu Asp Cys Val Ala Asp Pro Glu Gly Arg Pro Trp
         5525                5530                    5535

aca gat gac tcc tgg cgg cca ggg tgg act ctc gcg gat gcc acg gtc    16656
Thr Asp Asp Ser Trp Arg Pro Gly Trp Thr Leu Ala Asp Ala Thr Val
         5540                5545                    5550

cag gtg ccg ggc gac cac ttc tcg atg atg gac gag cac gcc ggg tcc    16704
Gln Val Pro Gly Asp His Phe Ser Met Met Asp Glu His Ala Gly Ser
         5555                5560                    5565

acc gca cag gca gtc gcg agt tgg ctt gac aaa ctc aac cag cgc acc    16752
Thr Ala Gln Ala Val Ala Ser Trp Leu Asp Lys Leu Asn Gln Arg Thr
     5570                5575                    5580

gct cgg caa cgc tga                                                16767
Ala Arg Gln Arg
5585


<210> 50
<211> 5588
<212> PRT
<213> Saccharopolyspora spinosa

<400> 50
Met Ala Asn Glu Glu Lys Leu Arg Glu Tyr Leu Lys Arg Val Val Val
1               5                   10                  15

Glu Leu Glu Glu Ala His Glu Arg Leu His Glu Leu Glu Arg Gln Glu
            20                  25                  30
```

His Asp Pro Ile Ala Ile Val Ser Met Gly Cys Arg Tyr Pro Gly Gly
        35   40   45

Val Ser Thr Pro Glu Glu Leu Trp Arg Leu Val Val Asp Gly Gly Asp
        50   55   60

Ala Ile Ala Asn Phe Pro Glu Asp Arg Gly Trp Asn Leu Asp Glu Leu
65   70   75   80

Phe Asp Pro Asp Pro Gly Arg Ala Gly Thr Ser Tyr Val Arg Glu Gly
                85   90   .   95

Gly Phe Leu Arg Gly Val Ala Asp Phe Asp Ala Gly Leu Phe Gly Ile
            100   105   110

Ser Pro Arg Glu Ala Gln Ala Met Asp Pro Gln Gln Arg Leu Leu Leu
            115   120   125

Glu Ile Ser Trp Glu Val Phe Glu Arg Ala Gly Ile Asp Pro Phe Ser
        130   135   140

Leu Arg Gly Thr Lys Thr Gly Val Phe Ala Gly Leu Ile Tyr His Asp
145   150   155   160

Tyr Ala Ser Arg Phe Arg Lys Thr Pro Ala Glu Phe Glu Gly Tyr Phe
                165   170   175

Ala Thr Gly Asn Ala Gly Ser Val Ala Ser Gly Arg Val Ala Tyr Thr
                180   185   190

Phe Gly Leu Glu Gly Pro Ala Val Thr Val Asp Thr Ala Cys Ser Ser
            195   200   205

Ser Leu Val Ala Leu His Leu Ala Cys Gln Ser Leu Arg Leu Gly Glu
        210   215   220

Cys Asp Leu Ala Leu Ala Gly Gly Ile Ser Val Met Ala Thr Pro Gly
225   230   235   240

Ala Phe Val Glu Phe Ser Arg Gln Arg Ala Leu Ala Ser Asp Gly Arg
                245   250   255

Cys Lys Pro Phe Ala Asp Ala Ala Asp Gly Thr Gly Trp Gly Glu Gly
            260   265   270

Ala Gly Met Leu Leu Leu Glu Arg Leu Ser Asp Ala Arg Arg Asn Gly
            275   280   285

301

```
His Pro Val Leu Ala Ala Val Val Gly Ser Ala Ile Asn Gln Asp Gly
    290             295             300

Thr Ser Asn Gly Leu Thr Ala Pro Ser Gly Pro Ala Gln Gln Arg Val
305             310             315             320

Ile Arg Gln Ala Leu Ala Asn Ala Gly Leu Ser Pro Ala Glu Val Asp
            325             330             335

Val Val Glu Ala His Gly Thr Gly Thr Ala Leu Gly Asp Pro Ile Glu
            340             345             350

Ala Gln Ala Leu Ile Ala Thr Tyr Gly Ala Asn Arg Ser Ala Asp His
            355             360             365

Pro Leu Leu Leu Gly Ser Leu Lys Ser Asn Ile Gly His Thr Gln Ala
    370             375             380

Ala Ala Gly Val Ala Gly Val Ile Lys Ser Val Leu Ala Ile Arg His
385             390             395             400

Arg Glu Met Pro Arg Ser Leu His Ile Asp Gln Pro Ser Gln His Val
            405             410             415

Asp Trp Ser Ala Gly Ala Val Arg Leu Leu Thr Asp Ser Val Asp Trp
            420             425             430

Pro Asp Leu Gly Arg Pro Arg Arg Ala Gly Val Ser Ser Phe Gly Met
    435             440             445

Ser Gly Thr Asn Ala His Leu Ile Val Glu Glu Val Ser Asp Glu Pro
    450             455             460

Val Ser Gly Ser Thr Glu Pro Thr Gly Ala Phe Pro Trp Pro Leu Ser
465             470             475             480

Gly Lys Thr Glu Thr Ala Leu Arg Glu Gln Ala Ala Glu Leu Leu Ser
            485             490             495

Val Val Thr Glu His Pro Glu Pro Gly Leu Gly Asp Val Gly Tyr Ser
            500             505             510

Leu Ala Thr Gly Arg Ala Ala Met Glu His Arg Ala Val Val Val Ala
            515             520             525

Asp Asp Arg Asp Ser Phe Val Ala Gly Leu Thr Ala Leu Ala Ala Gly
    530             535             540
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Val Pro Ala Ala Asn Val Val Gln Gly Ala Ala Asp Cys Lys Gly Lys
545             550             555             560

Val Ala Phe Val Phe Pro Gly Gln Gly Ser His Trp Gln Gly Met Ala
                565             570             575

Arg Glu Leu Ser Glu Ser Ser Pro Val Phe Arg Arg Lys Leu Ala Glu
            580             585             590

Cys Ala Ala Ala Thr Ala Pro Tyr Val Asp Trp Ser Leu Leu Gly Val
            595             600             605

Leu Arg Gly Asp Pro Asp Ala Pro Ala Leu Asp Arg Asp Asp Val Ile
        610             615             620

Gln Leu Ala Leu Phe Ala Met Met Val Ser Leu Ala Glu Leu Trp Arg
625             630             635             640

Ser Cys Gly Val Glu Pro Ala Ala Val Val Gly His Ser Gln Gly Glu
                645             650             655

Ile Ala Ala Ala His Val Ala Gly Ala Leu Ser Leu Thr Asp Ala Val
                660             665             670

Arg Ile Ile Ala Ala Arg Cys Asp Ala Val Ser Ala Leu Thr Gly Lys
            675             680             685

Gly Gly Met Leu Ala Ile Ala Leu Pro Glu Ser Ala Val Val Lys Arg
        690             695             700

Ile Ala Gly Leu Pro Glu Leu Thr Val Ala Ala Val Asn Gly Pro Gly
705             710             715             720

Ser Thr Val Val Ser Gly Glu Pro Ser Ala Leu Glu Arg Leu Gln Thr
                725             730             735

Glu Leu Thr Ala Glu Asn Val Gln Thr Arg Arg Val Gly Ile Asp Tyr
            740             745             750

Ala Ser His Ser Pro Gln Ile Ala Gln Val Gln Gly Arg Leu Leu Asp
            755             760             765

Arg Leu Gly Glu Val Gly Ser Glu Pro Ala Glu Ile Ala Phe Tyr Ser
        770             775             780

Thr Val Thr Gly Glu Arg Thr Asp Thr Gly Arg Leu Asp Ala Asp Tyr
785             790             795             800
```

303

Trp Tyr Gln Asn Leu Arg Gln Pro Val Arg Phe Gln Gln Thr Val Ala
            805   810   815

Arg Met Ala Asp Gln Gly Tyr Arg Phe Phe Val Glu Val Ser Pro His
            820   825   830

Pro Leu Leu Thr Ala Gly Ile Gln Glu Thr Leu Glu Ala Ala Asp Ala
            835   840   845

Gly Gly Val Val Val Gly Ser Leu Arg Arg Gly Glu Gly Gly Ser Arg
    850   855   860

Arg Trp Leu Thr Ser Leu Ala Glu Cys Gln Val Arg Gly Leu Pro Val
865   870   875   880

Asn Trp Glu Gln Val Phe Leu Asn Thr Gly Ala Arg Arg Val Pro Leu
            885   890   895

Pro Thr Tyr Pro Phe Gln Arg Gln Arg Tyr Trp Leu Glu Ser Ala Glu
            900   905   910

Tyr Asp Ala Gly Asp Leu Gly Ser Val Gly Leu Leu Ser Ala Glu His
    915   920   925

Pro Leu Leu Gly Ala Ala Val Thr Leu Ala Asp Ala Gly Gly Phe Leu
    930   935   940

Leu Thr Gly Lys Leu Ser Val Lys Thr Gln Pro Trp Leu Ala Asp His
945   950   955   960

Val Val Gly Gly Ala Ile Leu Leu Pro Gly Thr Ala Phe Val Glu Met
            965   970   975

Leu Ile Arg Ala Ala Asp Gln Val Gly Cys Asp Leu Ile Glu Glu Leu
            980   985   990

Ser Leu Thr Thr Pro Leu Val Leu Pro Ala Thr Gly Ala Val Gln Val
            995   1000   1005

Gln Ile Ala Val Gly Gly Pro Asp Glu Ala Gly Arg Arg Ser Val Arg
    1010   1015   1020

Val His Ser Cys Arg Asp Asp Ala Val Pro Gln Asp Ser Trp Thr Cys
025   1030   1035   1040

His Ala Thr Gly Thr Leu Thr Ser Ser Asp His Gln Asp Ala Gly Gln
            1045   1050   1055

Gly Pro Asp Gly Ile Trp Pro Pro Asn Asp Ala Val Ala Val Pro Leu
          1060   1065   1070

Asp Ser Phe Tyr Ala Arg Ala Ala Glu Arg Gly Phe Asp Phe Gly Pro
     1075   1080   1085

Ala Phe Gln Gly Leu Gln Ala Ala Trp Lys Arg Gly Asp Glu Ile Phe
     1090   1095   1100

Ala Glu Val Gly Leu Pro Thr Ala His Arg Glu Asp Ala Gly Arg Phe
105   1110   1115   1120

Gly Ile His Pro Ala Leu Leu Asp Ala Ala Leu Gln Ala Leu Gly Ala
          1125   1130   1135

Ala Glu Glu Asp Pro Asp Glu Gly Trp Leu Pro Phe Ala Trp Gln Gly
          1140   1145   ·   1150

Val Ser Leu Lys Ala Thr Gly Ala Leu Ser Leu Arg Val His Leu Val
          1155   1160   1165

Pro Ala Gly Ala Asn Ala Val Ser Val Phe Thr Thr Asp Thr Thr Gly
     1170   1175   1180

Gln Ala Val Leu Ser Ile Asp Ser Leu Val Leu Arg Gln Ile Ser Asp
185   1190   1195   1200

Lys Gln Leu Ala Ala Ala Arg Ala Met Glu His Glu Ser Leu Phe Arg
          1205   1210   1215

Val Asp Trp Lys Arg Ile Ser Pro Gly Ala Ala Lys Pro Val Ser Trp
          1220   1225   1230

Ala Val Ile Gly Asn Asp Glu Leu Ala Arg Ala Cys Gly Ser Ala Leu
          1235   1240   1245

Gly Thr Glu Leu His Pro Asp Leu Thr Gly Leu Ala Asp Pro Pro Pro
          1250   1255   1260

Asp Val Val Val Val Pro Cys Gly Ala Ser Arg Gln Asp Leu Asp Val
265   1270   1275   1280

Ala Ser Glu Ala Arg Ala Ala Thr Gln Arg Met Leu Asp Leu Ile Gln
          1285   1290   1295

Asp Trp Leu Ala Ala Ala Arg Phe Ala Gly Ser Arg Leu Val Val Val
          1300   1305   1310

Thr Cys Gly Ala Ala Ser Thr Gly Pro Ala Glu Gly Val Ser Asp Leu
        1315   1320   1325

Val His Ala Ala Ser Trp Gly Leu Leu Arg Ser Ala Gln Ser Glu Asn
        1330   1335   1340

Pro Asp Arg Phe Val Leu Val Asp Val Asp Gly Thr Ala Glu Ser Trp
345   1350   1355   1360

Arg Ala Leu Ala Ala Ala Val Arg Ser Gly Glu Pro Gln Leu Ala Leu
            1365   1370   1375

Arg Ala Gly Glu Val Arg Val Pro Arg Leu Ala Arg Cys Val Ala Ala
            1380   1385   1390

Glu Asp Ser Arg Ile Pro Val Pro Gly Ala Asp Gly Thr Val Leu Ile
        1395   1400   1405

Ser Gly Gly Thr Gly Leu Leu Gly Gly Leu Val Ala Arg His Leu Val
        1410   1415   1420

Ala Glu Arg Gly Val Arg Arg Leu Val Leu Ala Gly Arg Arg Gly Trp
425   1430   1435   1440

Ser Ala Pro Gly Val Thr Asp Leu Val Asp Glu Leu Val Gly Leu Gly
            1445   1450   1455

Ala Ala Val Glu Val Ala Ser Cys Asp Val Gly Asp Arg Ala Gln Leu
            1460   1465   1470

Asp Arg Leu Leu Thr Thr Ile Ser Ala Glu Phe Pro Leu Arg Gly Val
        1475   1480   1485

Val His Ala Ala Gly Ala Leu Ala Asp Gly Val Val Glu Ser Leu Thr
        1490   1495   1500

Pro Glu His Val Ala Lys Val Phe Gly Pro Lys Ala Ala Gly Ala Trp
505   1510   1515   · 1520

His Leu His Glu Leu Thr Leu Asp Leu Asp Leu Ser Phe Phe Val Leu
            1525   1530   1535

Phe Ser Ser Phe Ser Gly Val Ala Gly Ala Ala Gly Gln Gly Asn Tyr
        1540   1545   1550

Ala Ala Ala Asn Ala Phe Leu Asp Gly Leu Ala Gln His Arg Arg Thr
        1555   1560   1565

Ala Gly Leu Pro Ala Val Ser Leu Ala Trp Gly Leu Trp Glu Gln Pro
1570   1575   1580

Ser Gly Met Thr Gly Ala Leu Asp Ala Ala Gly Arg Ser Arg Ile Ala
585   1590   1595   1600

Arg Thr Asn Pro Pro Met Ser Ala Pro Asp Gly Leu Arg Leu Phe Glu
1605   1610   1615

Met Ala Phe Arg Val Pro Gly Glu Ser Leu Leu Val Pro Val His Val
1620   1625   1630

Asp Leu Asn Ala Leu Arg Ala Asp Ala Ala Asp Gly Gly Val Pro Ala
1635   1640   1645

Leu Leu Arg Asp Leu Val Pro Ala Pro Val Arg Arg Ser Ala Val Asn
1650   1655   1660

Glu Ser Ala Asp Val Asn Gly Leu Val Gly Arg Leu Arg Arg Leu Pro
665   1670   1675   1680

Asp Leu Asp Gln Glu Thr Gln Leu Leu Gly Leu Val Arg Glu His Val
1685   1690   1695

Ser Ala Val Leu Gly His Ser Gly Ala Val Glu Val Gly Ala Asp Arg
1700   1705   1710

Ala Phe Arg Asp Leu Gly Phe Asp Ser Leu Ser Gly Val Glu Phe Arg
1715   1720   1725

Asn Arg Leu Gly Gly Val Leu Gly Val Arg Leu Pro Ala Thr Ala Val
1730   1735   1740

Phe Asp Tyr Pro Thr Pro Arg Ala Leu Val Arg Phe Leu Leu Asp Lys
745   1750   1755   1760

Leu Ile Gly Gly Val Glu Ala Pro Thr Pro Ala Pro Ala Ala Val Ala
1765   1770   1775

Ala Val Thr Ala Asp Asp Pro Val Val Ile Val Gly Met Gly Cys Arg
1780   1785   1790

Tyr Pro Gly Gly Val Ser Ser Pro Glu Glu Leu Trp Arg Leu Val Ala
1795   1800   1805

Gly Gly Leu Asp Ala Val Ala Glu Phe Pro Asp Asp Arg Gly Trp Asp
1810   1815   1820

307

Gln Ala Gly Leu Phe Asp Pro Asp Pro Asp Arg Leu Gly Thr Ser Tyr
825   1830   1835   1840

Val Cys Glu Gly Gly Phe Leu Arg Asp Ala Ala Glu Phe Asp Ala Gly
              1845   1850   1855

Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln
          1860   1865   1870

Arg Leu Leu Leu Glu Val Ala Trp Glu Thr Val Glu Arg Ala Gly Ile
      1875   1880   1885

Asp Pro Leu Ser Leu Arg Gly Ser Arg Thr Gly Val Phe Ala Gly Leu
    1890   1895   1900

Met His His Asp Tyr Gly Ala Arg Phe Ile Thr Arg Ala Pro Glu Gly
905   1910   1915   1920

Phe Glu Gly Tyr Leu Gly Asn Gly Ser Ala Gly Gly Val Phe Ser Gly
          1925   1930   1935

Arg Val Ala Tyr Ser Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp
      1940   1945   1950

Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala Gly Gln Ala
      1955   1960   1965

Leu Arg Ser Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val
    1970   1975   1980

Met Ala Thr Pro Gly Met Phe Val Glu Phe Ser Arg Gln Arg Gly Leu
985   1990   1995   2000

Ala Ala Asp Gly Arg Cys Lys Ser Phe Ala Ala Ala Ala Asp Gly Thr
          2005   2010   2015

Gly Trp Gly Glu Gly Ala Gly Leu Val Leu Leu Glu Arg Leu Ser Asp
          2020   2025   2030

Ala Arg Arg Asn Gly His Ala Val Leu Ala Val Val Arg Gly Ser Ala
      2035   2040   2045

Val Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro
    2050   2055   2060

Ser Gln Gln Arg Val Ile Thr Gln Ala Leu Ala Ser Ala Gly Leu Ser
065   2070   2075   2080

308

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Val Ser Asp Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu
            2085                2090                2095

Gly Asp Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr Tyr Gly Gln Gly
            2100                2105                2110

Arg Asp Ser Asp Arg Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile
            2115              ' 2120                2125

Gly His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val
            2130                2135                2140

Met Ala Met Arg His Gly Gln Leu Pro Ala Thr Leu His Val Asp Glu
145                2150                2155                2160

Pro Thr Ser Glu Val Asp Trp Ser Ala Gly Asp Val Gln Leu Leu Thr
            2165                2170                2175

Glu Asn Thr Pro Trp Pro Gly Asn Ser His Pro Arg Arg Val Gly Val
            2180                2185                2190

Ser Ser Phe Gly Ile Ser Gly Thr Asn Ala His Val Ile Leu Glu Gln
            2195                2200                2205

Ala Ser Lys Thr Pro Asp Glu Thr Ala Asp Lys Ser Gly Pro Asp Ser
            2210                2215                2220

Glu Ser Thr Val Asp Leu Pro Ala Val Pro Leu Ile Val Ser Gly Arg
225                2230                2235                2240

Thr Pro Ala Ala Leu Ser Ala Gln Ala Ser Ala Leu Leu Ser Tyr Leu
            2245                2250                2255

Gly Glu Arg Gly Asp Ile Ser Thr Leu Asp Ala Ala Phe Ser Leu Ala
            2260                2265                2270

Ser Ser Arg Ala Ala Leu Glu Glu Arg Ala Val Val Leu Gly Ala Asp
            2275                2280                2285

Arg Glu Thr Leu Leu Ser Gly Leu Glu Ala Leu Ala Ser Gly Arg Glu
            2290                2295                2300

Ala Ser Gly Val Val Ser Gly Ser Pro Val Ser Gly Gly Val Gly Phe
305                2310                2315                2320

Val Phe Ala Gly Gln Gly Gly Gln Trp Leu Gly Met Gly Arg Gly Leu
            2325                2330                2335
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Tyr Ser Val Phe Pro Val Phe Ala Asp Ala Phe Asp Glu Ala Cys Ala
        2340              2345              2350

Gly Leu Asp Ala His Leu Gly Gln Asp Val Gly Val Arg Asp Val Val
        2355              2360              2365

Phe Gly Ser Asp Gly Ser Leu Leu Asp Arg Thr Leu Trp Ala Gln Ser
    2370              2375              2380

Gly Leu Phe Ala Leu Gln Val Gly Leu Leu Ser Leu Leu Gly Ser Trp
385               2390              2395              2400

Gly Val Arg Pro Gly Val Val Leu Gly His Ser Val Gly Glu Phe Ala
        2405              2410              2415

Ala Ala Val Ala Ala Gly Val Leu Ser Leu Pro Asp Ala Ala Arg Met
        2420              2425              2430

Val Ala Gly Arg Ala Arg Leu Met Gln Ala Leu Pro Ser Gly Gly Ala
        2435              2440              2445

Met Leu Ala Val Ala Ala Gly Glu Glu Gln Leu Arg Pro Leu Leu Ala
    2450              2455              2460

Asp Arg Val Asp Gly Ala Gly Ile Ala Ala Val Asn Ala Pro Glu Ser
465               2470              2475              2480

Val Val Leu Ser Gly Asp Arg Glu Val Leu Asp Asp Ile Ala Gly Ala
        2485              2490              2495

Leu Asp Gly Gln Gly Ile Arg Trp Arg Arg Leu Arg Val Ser His Ala
        2500              2505              2510

Phe His Ser Tyr Arg Met Asp Pro Met Leu Gln Glu Phe Ala Glu Ile
    2515              2520              2525

Ala Arg Ser Val Asp Tyr Arg Arg Gly Asp Leu Pro Val Val Ser Thr
    2530              2535              2540

Leu Thr Gly Glu Leu Asp Thr Ala Gly Val Met Ala Thr Pro Glu Tyr
545               2550              2555              2560

Trp Val Arg Gln Val Arg Glu Pro Val Arg Phe Ala Asp Gly Val Arg
        2565              2570              2575

Val Leu Ala Gln Gln Gly Val Ala Thr Ile Phe Glu Leu Gly Pro Asp
        2580              2585              2590
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                                    310

Ala Thr Leu Ser Ala Leu Ile Pro Asp Cys His Ser Trp Ala Asp Gln
    2595   2600   2605

Ala Met Pro Ile Pro Met Leu Arg Lys Asp Arg Thr Glu Thr Glu Thr
    2610   2615   2620

Val Val Ala Ala Val Ala Arg Ala His Thr Arg Gly Val Pro Val Glu
625   2630   2635   2640

Trp Ser Ala Tyr Phe Ala Gly Thr Gly Ala Arg Arg Val Glu Leu Pro
            2645   ·   2650   2655

Thr Tyr Ala Phe Gln Arg Gln Arg Tyr Trp Leu Glu Thr Ser Asp Tyr
            2660   2665   2670

Gly Asp Val Thr Gly Ile Gly Leu Ala Ala Ala Glu His Pro Leu Leu
    2675   2680   2685

Gly Ala Val Val Ala Leu Ala Asp Gly Asp Gly Met Val Leu Thr Gly
    2690   2695   2700

Arg Leu Ser Val Gly Thr His Pro Trp Leu Ala Gln His Arg Val Leu
705   2710   2715   2720

Gly Glu Val Val Val Pro Gly Thr Ala Ile Leu Glu Met Ala Leu His
            2725   2730   2735

Ala Gly Ala Arg Leu Gly Cys Asp Arg Val Glu Glu Leu Thr Leu Glu
            2740   2745   2750

Thr Pro Leu Val Val Pro Glu Arg Ala Ala Gly Ala Gly Ser Arg Gly
            2755   2760   2765

Pro Ala Gly Gly Thr Thr Val Ser Ile Glu Thr Ala Glu Glu Arg Val
    2770   2775   2780

Arg Thr Asn Asp Ala Ile Glu Ile Gln Leu Leu Val Asn Ala Pro Asp
785   2790   2795   2800

Glu Gly Gly Arg Arg Arg Val Ser Leu Tyr Ser Arg Pro Ala Gly Gly
            2805   2810   2815

Ser Arg Gly Gly Gly Trp Thr Arg His Ala Thr Gly Glu Leu Val Val
            2820   2825   2830

Gly Thr Thr Gly Gly Arg Ala Val Pro Asp Trp Ser Ala Glu Gly Ala
    2835   2840   2845

311

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Glu Ser Ile Ala Leu Asp Glu Phe Tyr Val Ala Leu Ala Gly Asn Gly
   2850                2855                2860

Phe Glu Tyr Gly Pro Leu Phe Gln Gly Leu Gln Ala Ala Trp Arg Arg
 865                2870                2875                2880

Gly Asp Glu Val Leu Ala Glu Ile Ala Pro Pro Ala Glu Ala Asp Ala
                2885                2890                2895

Met Ala Ser Gly Tyr Leu Leu Asp Pro Ala Leu·Leu Asp Ala Ala Leu
                2900                2905                2910

Gln Ala Ser Ala Leu Gly Asp Arg Pro Glu Gln Gly Gly Ala Trp Leu
                2915                2920                2925

Pro Phe Ser Phe Thr Gly Val Glu Leu Ser Ala Pro Ala Gly Thr Ile
   2930                2935                2940

Ser Arg Val Arg Leu Glu Thr Arg Arg Pro Asp Ala Ile Ser Val Ala
 945                2950                2955                2960

Val Met Asp Glu Ser Gly Arg Leu Leu Ala Ser Ile Asp Ser Leu Arg
                2965                2970                2975

Leu Arg Ser Val Ser Ser Gly Gln Leu Ala Asn Arg Asp Ala Val Arg
                2980                2985                2990

Asp Ala Leu Phe Glu Val Thr Trp Glu Pro Val Ala Thr Gln Ser Thr
   2995                3000                3005

Glu Pro Gly Arg Trp Ala Leu Leu Gly Asp Thr Ala Cys Gly Lys Asp
   3010                3015                3020

Asp Leu Ile Lys Leu Ala Thr Asp Ser Ala Asp Arg Cys Ala Asp Leu
 025                3030                3035                3040

Ala Ala Leu Ala Glu Lys Leu Asp Ser Ser Ala Leu Val Pro Asp Val
                3045                3050                3055

Val Val Tyr Cys Ala Gly Glu Gln Ala Asp Pro Gly Thr Gly Ala Ala
                3060                3065                3070

Ala Leu Ala Glu Thr Gln Gln Thr Leu Ala Leu Leu Gln Ala Trp Leu
   3075                3080                3085

Ala Glu Pro Arg Leu Ala Glu Ala Arg Leu Val Val Val Thr Cys Ala
   3090                3095                3100
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Ala Val Thr Thr Ala Pro Ser Asp Gly Ala Ser Glu Leu Ala His Ala
105               3110              3115              3120

Pro Leu Trp Gly Leu Leu Arg Ala Ala Gln Val Glu Asn Pro Gly Gln
              3125              3130              3135

Phe Val Leu Ala Asp Val Asp Gly Thr Ala Glu Ser Trp Arg Ala Leu
          3140              3145              3150

Pro Ser Ala Leu Gly Ser Met Glu Pro Gln Leu Ala Leu Arg Lys Gly
          3155              3160              3165

Ala Val Arg Ala Pro Arg Leu Ala Ser Val Ala Gly Gln Ile Asp Val
      3170              3175              3180

Pro Ala Val Val Ala Asp Pro Asp Arg Thr Val Leu Ile Ser Gly Gly
185               3190              3195              3200

Thr Gly Leu Leu Gly Gly Ala Val Ala Arg His Leu Val Thr Glu Arg
          3205              3210              3215

Gly Val Arg Arg Leu Val Leu Thr Gly Arg Arg Gly Trp Asp Ala Pro
          3220              3225              3230

Gly Ile Thr Glu Leu Val Gly Glu Leu Asn Gly Leu Gly Ala Val Val
      3235              3240              3245

Asp Val Val Ala Cys Asp Val Ala Asp Arg Ala Asp Leu Glu Ser Leu
      3250              3255              3260

Leu Ala Ala Val Pro Ala Glu Phe Pro Leu Cys Gly Val Val His Ala
265               3270              3275              3280

Ala Gly Ala Leu Ala Asp Gly Val Ile Glu Ser Leu Ser Pro Asp Asp
          3285              3290              3295

Val Gly Ala Val Phe Gly Pro Lys Ala Ala Gly Ala Trp Asn Leu His
          3300              3305              3310

Glu Leu Thr Arg Asp Thr Asp Leu Ser Phe Phe Ala Leu Phe Ser Ser
          3315              3320              3325

Leu Ser Gly Val Ala Gly Ala Pro Gly Gln Gly Asn Tyr Ala Ala Ala
      3330              3335              3340

Asn Ala Phe Leu Asp Ala Leu Ala His Tyr Arg Arg Ser Gln Gly Leu
345               3350              3355              3360
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313

Pro Ala Val Ser Leu Ala Trp Gly Leu Trp Glu Gln Pro Ser Gly Met
          3365   3370   3375

Thr Glu Thr Leu Ser Glu Val Asp Arg Ser Arg Ile Ala Arg Ala Asn
          3380   3385   3390

Pro Pro Leu Ser Thr Lys Glu Gly Leu Arg Leu Phe Asp Ala Gly Leu
          3395   3400   3405

Ala Leu Asp Arg Ala Ala Val Val Pro Ala Lys Leu Asp Arg Thr Phe
      3410   3415   3420

Leu Ala Glu Gln Ala Arg Ser Gly Ser Leu Pro Ala Leu Leu Thr Ala
425   3430   3435   3440

Leu Val Pro Pro Ile Arg Arg Asn Arg Arg Ala Ser Gly Thr Glu Leu
          3445   3450   3455

Ala Asp Glu Gly Thr Leu Leu Gly Val Val Arg Glu His Ala Ala Ala
          3460   3465   3470

Val Leu Gly Tyr Ser Ser Ala Ala Asp Val Gly Val Glu Arg Ala Phe
          3475   3480   3485

Arg Asp Leu Gly Phe Asp Ser Leu Ser Gly Val Glu Leu Arg Asn Arg
      3490   3495   3500

Leu Ala Gly Val Leu Gly Val Arg Leu Pro Ala Thr Ala Val Phe Asp
505   3510   3515   3520

Tyr Pro Thr Pro Arg Ala Leu Ala Arg Phe Leu His Gln Glu Leu Ala
          3525   3530   3535

Asp Glu Ile Ala Thr Thr Pro Ala Pro Val Thr Thr Thr Arg Ala Pro
          3540   3545   3550

Val Ala Glu Asp Asp Leu Val Ala Ile Val Gly Met Gly Cys Arg Phe
          3555   3560   3565

Pro Gly Gln Val Ser Ser Pro Glu Glu Leu Trp Arg Leu Val Ala Gly
      3570   3575   3580

Gly Val Asp Ala Val Ala Asp Phe Pro Ala Asp Arg Gly Trp Asp Leu
585   3590   3595   3600

Ala Gly Leu Phe Asp Pro Asp Pro Glu Arg Ala Gly Lys Thr Tyr Val
          3605   3610   3615

314

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Arg Glu Gly Ala Phe Leu Thr Asp Ala Asp Arg Phe Asp Ala Gly Phe
        3620                3625                3630

Phe Gly Ile Ser Pro Arg Glu Ala Leu Ala Met Asp Pro Gln Gln Arg
        3635                3640                3645

Leu Leu Leu Glu Leu Ser Trp Glu Ala Ile Glu Arg Ala Gly Ile Asp
    3650                3655                3660

Pro Gly Ser Leu Arg Gly Ser Arg Thr Gly Val Phe Ala Gly Leu Met
665                 3670                3675                3680

Tyr His Asp Tyr Gly Ala Arg Phe Ala Ser Arg Ala Pro Glu Gly Phe
            3685                3690                3695

Glu Gly Tyr Leu Gly Asn Gly Ser Ala Gly Ser Val Ala Ser Gly Arg
            3700                3705                3710

Ile Ala Tyr Ser Phe Gly Phe Glu Gly Pro Ala Val Thr Val Asp Thr
        3715                3720                3725

Ala Cys Ser Ser Ser Leu Val Ala Leu His Leu Ala Gly Gln Ser Leu
    3730                3735                3740

Arg Ser Gly Glu Cys Asp Leu Ala Leu Ala Gly Gly Val Thr Val Met
745                 3750                3755                3760

Ser Thr Pro Gly Thr Phe Val Glu Phe Ser Arg Gln Arg Gly Leu Ala
            3765                3770                3775

Pro Asp Gly Arg Cys Lys Ser Phe Ala Glu Ser Ala Asp Gly Thr Gly
            3780                3785                3790

Trp Gly Glu Gly Ala Gly Leu Val Leu Leu Glu Arg Leu Ser Asp Ala
        3795                3800                3805

Arg Arg Asn Gly His Arg Val Leu Ala Val Val Arg Gly Ser Ala Val
    3810                3815                3820

Asn Gln Asp Gly Ala Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro Ser
825                 3830                3835                3840

Gln Gln Arg Val Ile Gln Gln Ala Leu Ala Ser Ala Gly Leu Ser Val
            3845                3850                3855

Ser Asp Val Asp Ala Val Glu Ala His Gly Thr Gly Thr Arg Leu Gly
        3860                3865                3870
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315

Asp Pro Ile Glu Ala Gln Ala Leu Ile Ala Thr Tyr Gly Arg Asp Arg
    3875   3880   . 3885

Asp Pro Gly Arg Pro Leu Trp Leu Gly Ser Val Lys Ser Asn Ile Gly
    3890   3895   3900

His Thr Gln Ala Ala Ala Gly Val Ala Gly Val Ile Lys Met Val Met
905   3910   3915   3920

Ala Met Arg His Gly Gln Leu Pro Arg Thr Leu His Val Asp Ala Pro
                3925   3930   3935

Ser Ser Gln Val Asp Trp Ser Ala Gly Arg Val Gln Leu Leu Thr Glu
        ·   3940   3945   3950

Asn Thr Pro Trp Pro Asp Ser Gly Arg Pro Cys Arg Val Gly Val Ser
    3955   3960   3965

Ser Phe Gly Ile Ser Gly Thr Asn Ala His Val Ile Leu Glu Gln Ser
    3970   3975   3980

Thr Gly Gln Met Asp Gln Ala Ala Glu Pro Asp Ser Ser Pro Val Leu
985   3990   3995   4000

Asp Val Pro Val Val Pro Trp Val Val Ser Gly Lys Thr Pro Glu Ala
                4005   4010   4015

Leu Ser Ala Gln Ala Ala Thr Leu Ala Thr Tyr Leu Asp Gln Asn Val
            4020   4025   4030

Asp Val Ser Pro Leu Asp Val Gly Ile Ser Leu Ala Val Thr Arg Ser
        4035   4040   4045

Ala Leu Asp Glu Arg Ala Val Val Leu Gly Ser Asp Arg Asp Thr Leu
    4050   4055   4060

Leu Ser Gly Leu Asn Ala Leu Ala Ala Gly His Glu Ala Ala Gly Val
065   4070   4075   4080

Val Thr Gly Pro Val Gly Ile Gly Gly Arg Thr Gly Phe Val Phe Ala
            4085   4090   4095

Gly Gln Gly Gly Gln Trp Leu Gly Met Gly Arg Arg Leu Tyr Ser Glu
            4100   4105   4110

Phe Pro Ala Phe Ala Gly Ala Phe Asp Glu Ala Cys Ala Glu Leu Asp
    4115   4120   4125

316

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Ala Asn Leu Gly Arg Glu Val Gly Val Arg Asp Val Val Phe Gly Ser
    4130             4135             4140

Asp Glu Ser Leu Leu Asp Arg Thr Leu Trp Ala Gln Ser Gly Leu Phe
145             4150             4155             4160

Ala Leu Gln Val Gly Leu Trp Glu Leu Leu Gly Thr Trp Gly Val Arg
        4165             4170             4175

Pro Ser Val Val Leu Gly His Ser Val Gly Glu Leu Ala Ala Ala Phe
        4180             4185             4190

Ala Ala Gly Val Leu Ser Met Ala Glu Ala Ala Arg Leu Val Ala Gly
        4195             4200             4205

Arg Ala Arg Leu Met Gln Ala Leu Pro Ser Gly Gly Ala Met Leu Ala
    4210             4215             4220

Val Ser Ala Thr Glu Ala Arg Val Gly Pro Leu Leu Asp Gly Val Arg
225             4230             4235             4240

Asp Arg Val Gly Val Ala Ala Val Asn Ala Pro Gly Ser Val Val Leu
        4245             4250             4255

Ser Gly Asp Arg Asp Val Leu Asp Gly Ile Ala Gly Arg Leu Asp Gly
        4260             4265             4270

Gln Gly Ile Arg Ser Arg Trp Leu Arg Val Ser His Ala Phe His Ser
    4275             4280             4285

His Arg Met Asp Pro Met Leu Ala Glu Phe Ala Glu Leu Ala Arg Ser
    4290             4295             4300

Val Asp Tyr Arg Ser Pro Arg Leu Pro Ile Val Ser Thr Leu Thr Gly
305             4310             4315             4320

Asn Leu Asp Asp Val Gly Val Met Ala Thr Pro Glu Tyr Trp Val Arg
        4325             4330             4335

Gln Val Arg Glu Pro Val Arg Phe Ala Asp Gly Val Gln Ala Leu Val
        4340             4345             4350

Asp Gln Gly Val Asp Thr Ile Val Glu Leu Gly Pro Asp Gly Ala Leu
        4355             4360             4365

Ser Ser Leu Val Gln Glu Cys Val Ala Glu Ser Gly Arg Ala Thr Gly
    4370             4375             4380
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Ile Pro Leu Val Arg Arg Asp Arg Asp Glu Val Arg Thr Val Leu Asp
385   4390   4395   4400

Ala Leu Ala Gln Thr His Thr Arg Gly Gly Ala Val Asp Trp Gly Ser
            4405   4410   4415

Phe Phe Ala Gly Thr Arg Ala Thr Gln Val Asp Leu Pro Thr Tyr Ala
            4420   4425   4430

Phe Gln Arg Gln Arg Tyr Trp Leu Glu Pro Ser Asp Ser Gly Asp Val
            4435   4440   4445

Thr Gly Val Gly Leu Thr Gly Ala Glu His Pro Leu Leu Gly Ala Val
            4450   4455   4460

Val Pro Val Ala Gly Gly Asp Glu Val Leu Leu Thr Gly Arg Leu Ser
465   4470   4475   4480

Val Gly Thr His Pro Trp Leu Ala Glu His Arg Val Leu Gly Glu Val
            4485   4490   4495

Val Val Pro Gly Thr Ala Leu Leu Glu Met Ala Trp Arg Ala Gly Ser
            4500   4505   4510

Gln Val Gly Cys Glu Arg Val Glu Glu Leu Thr Leu Glu Ala Pro Leu
            4515   4520   4525

Val Leu Pro Glu Arg Gly Ala Ala Ala Val Gln Leu Ala Val Gly Ala
            4530   4535   4540

Pro Asp Glu Ala Gly Arg Arg Ser Leu Gln Leu Tyr Ser Arg Gly Ala
545   4550   4555   4560

Asp Glu Asp Gly Asp Trp Arg Arg Ile Ala Ser Gly Leu Leu Ala Gln
            4565   4570   4575

Ala Asn Ala Val Pro Pro Ala Asp Ser Thr Ala Trp Pro Pro Asp Gly
            4580   4585   4590

Ala Gly Gln Val Asp Leu Ala Glu Phe Tyr Glu Arg Leu Ala Glu Arg
            4595   4600   4605

Gly Leu Thr Tyr Gly Pro Val Phe Gln Gly Leu Arg Ala Ala Trp Arg
            4610   4615   4620

His Gly Asp Asp Ile Phe Ala Glu Leu Ala Gly Ser Pro Asp Ala Ser
625   4630   4635   4640

Gly Phe Gly Ile His Pro Ala Leu Leu Asp Ala Ala Leu His Ala Met
        4645   4650   4655   .

Ala Leu Gly Ala Ser Pro Asp Ser Glu Ala Arg Leu Pro Phe Ser Trp
        4660   4665   4670

Arg Gly Ala Gln Leu Tyr Arg Ala Glu Gly Ala Ala Leu Arg Val Arg
        4675   4680   4685
                                                        .

Leu Ser Pro Leu Gly Ser Gly Ala Val Ser Leu Thr Leu Val Asp Ala
        4690   .   4695   4700

Thr Gly Arg Arg Val Ala Ala Val Glu Ser Leu Ser Thr Arg Pro Val
705   4710   4715   4720
                                     .

Ser Thr Asp Gln Ile Gly Ala Gly Arg Gly Asp Gln Glu Arg Leu Leu
        4725   4730   4735

His Val Glu Trp Val Arg Ser Ala Glu Ser Ala Gly Met Ser Leu Thr
        4740   4745   4750

Ser Cys Ala Val Val Gly Leu Gly Glu Pro Glu Trp His Ala Ala Leu
        4755   4760   4765

Lys Thr Thr Gly Val Gln Val Glu Ser His Ala Asp Leu Ala Ser Leu
        4770   4775   4780

Ala Thr Glu Val Ala Lys Arg Gly Ser Ala Pro Gly Ala Val Ile Val
785   4790   4795   4800

Pro Cys Pro Arg Pro Arg Ala Met Gln Glu Leu Pro Thr Ala Ala Arg
            4805   4810   4815

Arg Ala Thr Gln Gln Ala Met Ala Met Leu Gln Gln Trp Leu Ala Asp
        4820   4825   4830

Asp Arg Phe Val Ser Thr Arg Leu Ile Leu Leu Thr His Arg Ala Val
        4835   4840   4845

Ser Ala Val Ala Gly Glu Asp Val Leu Asp Leu Val His Ala Pro Leu
    4850   4855   4860

Trp Gly Leu Val Arg Ser Ala Gln Ala Glu His Pro Asp Arg Phe Ala
865   4870   4875   4880

Leu Ile Asp Met Asp Asp Glu Arg Ala Ser Gln Thr Ala Leu Ala Glu
        4885   4890   4895

319

Ala Leu Thr Ala Gly Glu Ala Gln Leu Ala Val Arg Ser Gly Val Val
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Leu Ala Pro Arg Leu Gly Gln Val Lys Val Ser Gly Gly Glu Ala Phe
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Arg Trp Asp Glu Gly Thr Val Leu Val Thr Gly Gly Thr Gly Gly Leu
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Gly Ala Leu Leu Ala Arg His Leu Val Ser Ala His Gly Val Arg His
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Leu Leu Leu Ala Ser Arg Arg Gly Leu Ala Ala Pro Gly Ala Asp Glu
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Leu Val Ala Glu Leu Glu Gln Ala Gly Ala Asp Val Ala Val Val Ala
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Cys Asp Ser Ala Asp Arg Asp Ser Leu Ala Arg Leu Val Ala Ser Val
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Pro Ala Glu Asn Pro Leu Arg Val Val Val His Ala Ala Gly Val Leu
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Asp Asp Gly Val Leu Met Ser Met Ser Pro Glu Arg Leu Asp Ala Val
025   5030   5035   5040

Leu Arg Pro Lys Val Asp Ala Ala Trp Tyr Leu His Glu Leu Thr Arg
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Glu Leu Gly Leu Ser Ala Phe Val Leu Phe Ser Ser Val Ala Gly Leu
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Phe Gly Gly Ala Gly Gln Ser Asn Tyr Ala Ala Gly Asn Ala Phe Leu
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Asp Ala Leu Ala His Cys Arg Gln Ala Gln Gly Leu Pro Ala Leu Ser
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Leu Ala Ser Gly Leu Trp Ala Ser Ile Asp Gly Met Ala Gly Asp Leu
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Ala Ala Ala Asp Val Glu Arg Leu Ser Arg Ala Gly Ile Gly Pro Leu
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Ser Ala Pro Gly Gly Leu Ala Leu Phe Asp Ala Ala Val Gly Ser Asp
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320

Glu Pro Leu Leu Ala Pro Val Arg Leu Asp Val Glu Ala Leu Arg Val
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Gln Ala Arg Ser Val Gln Thr Arg Ile Pro Glu Met Leu His Gly Met
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Ala Met Gly Pro Ser Arg Arg Thr Pro Phe Thr Ser Arg Val Glu Pro
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Val Leu Gln Arg Val Arg Ala Asp Ile Ala Val Val Leu Gly His Gly
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Arg Ser Ser Asp Val Asp Ile Glu Lys Pro Leu Ala Glu Leu Gly Phe
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Asp Ser Leu Thr Ala Ile Glu Leu Arg Asn Arg Leu Ala Thr Ala Thr
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Gly Leu Arg Leu Pro Ala Thr Leu Ala Phe Asp His Gly Thr Ala Ala
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Ala Leu Ala Gln His Val Cys Ala Gln Leu Gly Thr Ala Thr Ala Pro
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Ala Pro Arg Arg Thr Asp Asp Asn Asp Ala Thr Glu Pro Val Arg Ser
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Leu Phe Gln Gln Ala Tyr Ala Ala Gly Arg Ile Leu Asp Gly Met Asp
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Leu Val Lys Val Ala Ala Gln Leu Arg Pro Val Phe Gly Ser Pro Gly
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Glu Leu Glu Ser Leu Pro Lys Pro Val Gln Leu Ser Arg Gly Pro Glu
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Glu Leu Ala Leu Val Cys Met Pro Ala Leu Ile Gly Met Pro Pro Ala
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Gln Gln Tyr Ala Arg Ile Ala Ala Gly Phe Arg Asp Val Arg Asp Val
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Ser Val Ile Pro Met Pro Gly Phe Ile Ala Gly Glu Pro Leu Pro Ser
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321

Ala Ile Glu Val Ala Val Arg Thr Gln Ala Glu Ala Val Leu Gln Glu
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Phe Ala Gly Gly Ser Phe Val Leu Val Gly His Ser Ser Gly Gly Trp
425   5430   5435 .   5440

Leu Ala His Glu Val Ala Gly Glu Leu Glu Arg Arg Gly Val Val Pro
              5445   5450   5455

Ala Gly Val Val Leu Leu Asp Thr Tyr Ile Pro Gly Glu Ile Thr Pro
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Arg Phe Ser Val Ala Met Ala His Arg Thr Tyr Glu Lys Leu Ala Thr
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Phe Thr Asp Met Gln Asp Val Gly Ile Thr Ala Met Gly Gly Tyr Phe
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Phe Val Arg Thr Glu Asp Cys Val Ala Asp Pro Glu Gly Arg Pro Trp
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Thr Asp Asp Ser Trp Arg Pro Gly Trp Thr Leu Ala Asp Ala Thr Val
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Gln Val Pro Gly Asp His Phe Ser Met Met Asp Glu His Ala Gly Ser
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323

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gtg gtc gtg ctc gac aag ctc acc tac gcc ggc aac gag gcg aac ctg   144
Val Val Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Glu Ala Asn Leu
            35                  40                  45

gcg ccg gtc gcg gac aac ccc cgg ctg aag ttc gtc tgc ggc gac atc   192
Ala Pro Val Ala Asp Asn Pro Arg Leu Lys Phe Val Cys Gly Asp Ile
        50                  55                  60

tgc gac cgc gaa ctg gtt ggc ggc ctg atg tcc ggc gtg gac gtg gtg   240
Cys Asp Arg Glu Leu Val Gly Gly Leu Met Ser Gly Val Asp Val Val
65                  70                  75                  80

gtg cac ttc gcc gcc gaa acc cac gtc gac cgc tcg atc acc ggc tcg   288
Val His Phe Ala Ala Glu Thr His Val Asp Arg Ser Ile Thr Gly Ser
                85                  90                  95

gac gcc ttc gtg atc acc aac gtg gtc ggc acc aac gtg ctg ctg cag   336
Asp Ala Phe Val Ile Thr Asn Val Val Gly Thr Asn Val Leu Leu Gln
                100                 105                 110

gcc gcg ctc gac gcc gag atc ggc aag ttc gtg cac gtt tcc acc gac   384
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            115                 120                 125

gag gtc tac ggc tcc atc gag gac ggc tcg tgg ccc gaa gac cac gcg   432
Glu Val Tyr Gly Ser Ile Glu Asp Gly Ser Trp Pro Glu Asp His Ala
        130                 135                 140

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145                 150                 155                 160

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ccg ctg ttc atc acg aac ctg atg gac ggc agc cag gtg ccg ctc tac   624
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ggc gac ggg ctc aac gtg cgg gac tgg ctg cac gtc agc gac cac tgc   672
Gly Asp Gly Leu Asn Val Arg Asp Trp Leu His Val Ser Asp His Cys
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cgg ggc atc cag ctg gtg gcc gac tcc ggg cgc gcg ggc gag atc tac   720
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225                    230                    235                    240

aac atc ggc ggc ggc acc gag ctg acc aac aac gag ctg acc gag cgg   768
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                245          .         250                    255

ctg ctg gca gag ctg ggc ctc gac tgg tcg gtg gtg cgg ccg gtc acc   816
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gtc gag gaa ctg ggg tac gcg ccg cag gtc gac ttc gag acc ggg ctg   912
Val Glu Glu Leu Gly Tyr Ala Pro Gln Val Asp Phe Glu Thr Gly Leu
                290                    295                    300

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Cys Asp Arg Glu Leu Val Gly Gly Leu Met Ser Gly Val Asp Val Val
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Val His Phe Ala Ala Glu Thr His Val Asp Arg Ser Ile Thr Gly Ser
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Asp Ala Phe Val Ile Thr Asn Val Val Gly Thr Asn Val Leu Leu Gln
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Ala Ala Leu Asp Ala Glu Ile Gly Lys Phe Val His Val Ser Thr Asp
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　　　　130　　　　　　　135　　　　　　　140

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Arg Cys Ser Asn Asn Tyr Gly Pro Tyr Gln Phe Pro Glu Lys Val Leu
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Pro Leu Phe Ile Thr Asn Leu Met Asp Gly Ser Gln Val Pro Leu Tyr
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Gly Asp Gly Leu Asn Val Arg Asp Trp Leu His Val Ser Asp His Cys
　　　　210　　　　　　　215　　　　　　　220

Arg Gly Ile Gln Leu Val Ala Asp Ser Gly Arg Ala Gly Glu Ile Tyr
225　　　　　　　230　　　　　　　235　　　　　　　240

Asn Ile Gly Gly Gly Thr Glu Leu Thr Asn Asn Glu Leu Thr Glu Arg
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Leu Leu Ala Glu Leu Gly Leu Asp Trp Ser Val Val Arg Pro Val Thr
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326

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Asp Arg Lys Gly His Asp Arg Arg Tyr Ser Val Asp His Ser Lys Ile
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Val Glu Glu Leu Gly Tyr Ala Pro Gln Val Asp Phe Glu Thr Gly Leu
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Arg Glu Thr Ile Arg Trp Tyr Gln Asp Asn Arg Asp Trp Trp Glu Pro
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Leu Lys Ala Arg Ser Ala Val Ala Arg
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tcg gag ctg gcc cgg atc ctc ccc gcg cgg acg ggg gcg ctg gtg cac      96
Ser Glu Leu Ala Arg Ile Leu Pro Ala Arg Thr Gly Ala Leu Val His
                20                  25                  30

cgg ccg ggt tcc ggg gaa ctg gac gtc acc gac gcc gag gag gtc gcc     144
Arg Pro Gly Ser Gly Glu Leu Asp Val Thr Asp Ala Glu Glu Val Ala
            35                  40                  45

gac gcg ttg ggt tcc ttc gcg gag acg gcg aag gac gcg gag ctg cga     192
Asp Ala Leu Gly Ser Phe Ala Glu Thr Ala Lys Asp Ala Glu Leu Arg
        50                  55                  60

ccg gtg gtg atc aac gcc gcg gcg tac acg gcg gtg gac gcg gcc gag     240
Pro Val Val Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Ala Ala Glu
65                  70                  75                  80

tcc gac ccg gac cgc gcg gcc cgg atc aac gcc gaa ggc gcg gcc tcg     288
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                85                  90                  95
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327

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ctg gcg aaa gcg tgc cgg agc agc ggt ctg ccc ctg gtg cac gtg tcg      336
Leu Ala Lys Ala Cys Arg Ser Ser Gly Leu Pro Leu Val His Val Ser
            100              105              110

acg gat tac gtg ttc ccc ggt gat ggg gcc cgg ccg tac gag ccg acg      384
Thr Asp Tyr Val Phe Pro Gly Asp Gly Ala Arg Pro Tyr Glu Pro Thr
            115              120              125

gac ccg acc ggg ccg cga tcg gtc tac ggg cgc acc aag ctc gaa ggc      432
Asp Pro Thr Gly Pro Arg Ser Val Tyr Gly Arg Thr Lys Leu Glu Gly
    130              135              140

gaa cgg gcc gtg ctg gag tcc ggc gcg cgg gcc tgg gtg gtg cgc acg      480
Glu Arg Ala Val Leu Glu Ser Gly Ala Arg Ala Trp Val Val Arg Thr
145              150              155              160

gca tgg gtg tac ggc gcg agc ggc aag aac ttc ctg aaa acg atg atc      528
Ala Trp Val Tyr Gly Ala Ser Gly Lys Asn Phe Leu Lys Thr Met Ile
                165              170              175

cgc ctc tcg ggg gag cgc gac acg ctg tcc gtt gtg gac gat cag atc      576
Arg Leu Ser Gly Glu Arg Asp Thr Leu Ser Val Val Asp Asp Gln Ile
            180              185              190

ggc tcg ccg act tgg gcg gcg gac ctg gcg agc ggc ctg ctg gag ctg      624
Gly Ser Pro Thr Trp Ala Ala Asp Leu Ala Ser Gly Leu Leu Glu Leu
            195              200              205

gcc gaa cgg gtc gcc gaa cgc cgt gga ccg gag cag aag gtg ctg cac      672
Ala Glu Arg Val Ala Glu Arg Arg Gly Pro Glu Gln Lys Val Leu His
    210              215              220

tgc acc aat tcc ggc cag gtg acc tgg tac gag ttc gcg cgg gcg atc      720
Cys Thr Asn Ser Gly Gln Val Thr Trp Tyr Glu Phe Ala Arg Ala Ile
225              230              235              240

ttc gcg gaa ttc ggc ctg gac gag aac cgc gtc cac ccg tgc acg acg      768
Phe Ala Glu Phe Gly Leu Asp Glu Asn Arg Val His Pro Cys Thr Thr
                245              250              255

gcg gac ttc ccc ctc ccg gcg cac cgc ccg gcc tac tcg gtc ctg tcc      816
Ala Asp Phe Pro Leu Pro Ala His Arg Pro Ala Tyr Ser Val Leu Ser
                260              265              270

gac gtg gcg tgg cga gag gcg ggc ctg acc ccg atg cgc acc tgg cgg      864
Asp Val Ala Trp Arg Glu Ala Gly Leu Thr Pro Met Arg Thr Trp Arg
            275              280              285
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gaa gcc ctg gcg gcg gcc ttc gag aaa gac ggc gaa acc ctc cga acc   912
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Arg
305
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Arg Pro Gly Ser Gly Glu Leu Asp Val Thr Asp Ala Glu Glu Val Ala
        35              40              45

Asp Ala Leu Gly Ser Phe Ala Glu Thr Ala Lys Asp Ala Glu Leu Arg
    50              55              60

Pro Val Val Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Ala Ala Glu
65              70              75              80

Ser Asp Pro Asp Arg Ala Ala Arg Ile Asn Ala Glu Gly Ala Ala Ser
            85              90              95

Leu Ala Lys Ala Cys Arg Ser Ser Gly Leu Pro Leu Val His Val Ser
            100             105             110

Thr Asp Tyr Val Phe Pro Gly Asp Gly Ala Arg Pro Tyr Glu Pro Thr
            115             120             125

Asp Pro Thr Gly Pro Arg Ser Val Tyr Gly Arg Thr Lys Leu Glu Gly
    130             135             140

Glu Arg Ala Val Leu Glu Ser Gly Ala Arg Ala Trp Val Val Arg Thr
145             150             155             160

Ala Trp Val Tyr Gly Ala Ser Gly Lys Asn Phe Leu Lys Thr Met Ile
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Arg Leu Ser Gly Glu Arg Asp Thr Leu Ser Val Val Asp Asp Gln Ile
            180               185               190

Gly Ser Pro Thr Trp Ala Ala Asp Leu Ala Ser Gly Leu Leu Glu Leu
            195               200               205

Ala Glu Arg Val Ala Glu Arg Arg Gly Pro Glu Gln Lys Val Leu His
        210               215               220

Cys Thr Asn Ser Gly Gln Val Thr Trp Tyr Glu Phe Ala Arg Ala Ile
225               230               235               240

Phe Ala Glu Phe Gly Leu Asp Glu Asn Arg Val His Pro Cys Thr Thr
                245               250               255

Ala Asp Phe Pro Leu Pro Ala His Arg Pro Ala Tyr Ser Val Leu Ser
            260               265               270

Asp Val Ala Trp Arg Glu Ala Gly Leu Thr Pro Met Arg Thr Trp Arg
            275               280               285

Glu Ala Leu Ala Ala Ala Phe Glu Lys Asp Gly Glu Thr Leu Arg Thr
        290               295               300

Arg
305
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(54) Title: NUCLEIC ACIDS WHICH CODE FOR THE ENZYME ACTIVITIES OF THE SPINOSYN BIOSYNTHESIS

(54) Bezeichnung: NUCLEINSÄUREN, DIE FÜR ENZYMAKTIVITÄTEN DER SPINOSYN-BIOSYNTHESE CODIEREN

(57) Abstract: The present invention relates to nucleic acids which code for the enzyme activities of the spinosyn biosynthesis. The invention also relates to the corresponding enzymes as such. The invention further relates to a method for producing spinosyn derivatives and spinosyn precursors.

(57) Zusammenfassung: Die vorliegende Erfindung betrifft Nucleinsäuren, die für Enzymaktivitäten der Spinosyn-Biosynthese codieren, sowie die entsprechenden Enzyme per se. Weiterhin betrifft die Erfindung Verfahren zum Herstellen von Spinosyn-Derivaten und -Vorstufen.

INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7   C12N15/52   C12N15/70   C12N1/21   C12N5/14   C07K14/195
C12P19/62

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7   C07K   C12N   C12P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	KIRST, H.A. ET AL.,: "Discovery, Isolation, and Structure Elucidation of a Family of Structurally Unique, Fermentation-Derived Tetracyclic Macrolides." 1992 , BAKER, D.R., FENYES, J.G. AND STEFFENS J.J. , AMERICAN CHEMICAL SOCIETY SYMPOSIUM SERIES NR. 504: SYNTHESIS AND CHEMISTRY OF AGROCHEMICALS III. WASHINGTON DC XP000944494 page 214 -page 255 the whole document --- -/--	1-6, 13-17, 19-32, 63-69

[X] Further documents are listed in the continuation of box C.   [X] Patent family members are listed in annex.

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"E" earlier document but published on or after the international filing date

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
15 December 2000	2 2. 02. 01

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Morawetz, R

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MATSUSHIMA P ET AL: "Conjugal transfer of cosmid DNA from Escherichia coli to Saccharopolyspora spinosa: effects of chromosomal insertions on macrolide A83543 production" GENE,NL,ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, vol. 146, no. 1, 1994, pages 39-45, XP002106258 ISSN: 0378-1119 the whole document	1-9,11, 13-33, 63-69
Y	HOPWOOD D A: "Genetic contributions to understanding polyketid synthases" CHEMICAL REVIEWS,US,AMERICAN CHEMICAL SOCIETY. EASTON, vol. 97, no. 7, November 1997 (1997-11), pages 2465-2497, XP002130647 ISSN: 0009-2665 the whole document	1-9,11, 13-33, 63-69
A	BALTZ R H ET AL: "Molecular genetic methods for improving secondary-metabolite production in actinomycetes" TRENDS IN BIOTECHNOLOGY,GB,ELSEVIER PUBLICATIONS, CAMBRIDGE, vol. 14, no. 7, 1 July 1996 (1996-07-01), pages 245-250, XP004035763 ISSN: 0167-7799 the whole document	
P,X	WO 99 46387 A (BROUGHTON M CHRISTINE ;MADDURI KRISHNAMURTHY (US); WALDRON CLIVE () 16 September 1999 (1999-09-16) the whole document	1-9,11, 13-33, 63-69

3

INTERNATIONAL SEARCH REPORT

Box I	Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II	Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-9, 11. 13-33, 63-69 (all in part)

Remark on Protest   ☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet (1)) (July 1992)

1. Claims Nos. 1-9, 11, 13-33, 63-69 (all in part)

   Nucleic acid according to SEQ ID NO: 7, gene product which can be derived therefrom, vector comprising at least the nucleic acid according to SEQ ID NO: 7, host cell containing a nucleic acid according to SEQ ID NO: 7, antibody which specifically reacts with the gene product, and method for producing the nucleic acid, the polypeptide or spinosyn.

2. Claims Nos. 1-9, 11, 13-31, 34, 35, 63-69 (all in part)

   Gene product like Invention No. 1, however, which can be derived for the nucleic acid according to SEQ ID NO: 9, and subject matter related thereto.

3. Claims Nos. 1-72 (all in part and if applicable) – 24. Claim Nos. 1-72 (all in part and if applicable)

   Gene products like Invention No. 1, however, which can be derived for the nucleic acid according to SEQ ID NO: 11 to SEQ ID NO: 54, and subject matter related thereto.

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 9946387	A	16-09-1999	US	6143526 A	07-11-2000
			AU	2680099 A	27-09-1999
			BR	9909257 A	28-11-2000
			EP	1062345 A	27-12-2000

INTERNATIONALER RECHERCHENBERICHT

A. KLASSIFIZIERUNG DES ANMELDUNGSGEGENSTANDES
IPK 7 C12N15/52 C12N15/70 C12N1/21 C12N5/14 C07K14/195
C12P19/62

Nach der Internationalen Patentklassifikation (IPK) oder nach der nationalen Klassifikation und der IPK

B. RECHERCHIERTE GEBIETE

Recherchierter Mindestprüfstoff (Klassifikationssystem und Klassifikationssymbole)
IPK 7 C07K C12N C12P

Recherchierte aber nicht zum Mindestprüfstoff gehörende Veröffentlichungen, soweit diese unter die recherchierten Gebiete fallen

Während der Internationalen Recherche konsultierte elektronische Datenbank (Name der Datenbank und evtl. verwendete Suchbegriffe)

C. ALS WESENTLICH ANGESEHENE UNTERLAGEN

Kategorie°	Bezeichnung der Veröffentlichung, soweit erforderlich unter Angabe der in Betracht kommenden Teile	Betr. Anspruch Nr.
X	KIRST, H.A. ET AL.,: "Discovery, Isolation, and Structure Elucidation of a Family of Structurally Unique, Fermentation-Derived Tetracyclic Macrolides." 1992 , BAKER, D.R., FENYES, J.G. AND STEFFENS J.J. , AMERICAN CHEMICAL SOCIETY SYMPOSIUM SERIES NR. 504: SYNTHESIS AND CHEMISTRY OF AGROCHEMICALS III. WASHINGTON DC XP000944494 Seite 214 -Seite 255 das ganze Dokument --- -/--	1-6, 13-17, 19-32, 63-69

[X] Weitere Veröffentlichungen sind der Fortsetzung von Feld C zu entnehmen

[X] Siehe Anhang Patentfamilie

° Besondere Kategorien von angegebenen Veröffentlichungen :

"A" Veröffentlichung, die den allgemeinen Stand der Technik definiert, aber nicht als besonders bedeutsam anzusehen ist

"E" älteres Dokument, das jedoch erst am oder nach dem internationalen Anmeldedatum veröffentlicht worden ist

"L" Veröffentlichung, die geeignet ist, einen Prioritätsanspruch zweifelhaft erscheinen zu lassen, oder durch die das Veröffentlichungsdatum einer anderen im Recherchenbericht genannten Veröffentlichung belegt werden soll oder die aus einem anderen besonderen Grund angegeben ist (wie ausgeführt)

"O" Veröffentlichung, die sich auf eine mündliche Offenbarung, eine Benutzung, eine Ausstellung oder andere Maßnahmen bezieht

"P" Veröffentlichung, die vor dem internationalen Anmeldedatum, aber nach dem beanspruchten Prioritätsdatum veröffentlicht worden ist

"T" Spätere Veröffentlichung, die nach dem internationalen Anmeldedatum oder dem Prioritätsdatum veröffentlicht worden ist und mit der Anmeldung nicht kollidiert, sondern nur zum Verständnis des der Erfindung zugrundeliegenden Prinzips oder der ihr zugrundeliegenden Theorie angegeben ist

"X" Veröffentlichung von besonderer Bedeutung; die beanspruchte Erfindung kann allein aufgrund dieser Veröffentlichung nicht als neu oder auf erfinderischer Tätigkeit beruhend betrachtet werden

"Y" Veröffentlichung von besonderer Bedeutung; die beanspruchte Erfindung kann nicht als auf erfinderischer Tätigkeit beruhend betrachtet werden, wenn die Veröffentlichung mit einer oder mehreren anderen Veröffentlichungen dieser Kategorie in Verbindung gebracht wird und diese Verbindung für einen Fachmann naheliegend ist

"&" Veröffentlichung, die Mitglied derselben Patentfamilie ist

Datum des Abschlusses der internationalen Recherche	Absendedatum des internationalen Recherchenberichts
15. Dezember 2000	2 2. 02. 01

Name und Postanschrift der Internationalen Recherchenbehörde	Bevollmächtigter Bediensteter
Europäisches Patentamt, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Morawetz, R

3

Formblatt PCT/ISA/210 (Blatt 2) (Juli 1992)

C.(Fortsetzung) ALS WESENTLICH ANGESEHENE UNTERLAGEN		
Kategorie°	Bezeichnung der Veröffentlichung, soweit erforderlich unter Angabe der in Betracht kommenden Teile	Betr. Anspruch Nr.
Y	MATSUSHIMA P ET AL: "Conjugal transfer of cosmid DNA from Escherichia coli to Saccharopolyspora spinosa: effects of chromosomal insertions on macrolide A83543 production" GENE,NL,ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, Bd. 146, Nr. 1, 1994, Seiten 39-45, XP002106258 ISSN: 0378-1119 das ganze Dokument ---	1-9,11, 13-33, 63-69
Y	HOPWOOD D A: "Genetic contributions to understanding polyketid synthases" CHEMICAL REVIEWS,US,AMERICAN CHEMICAL SOCIETY. EASTON, Bd. 97, Nr. 7, November 1997 (1997-11), Seiten 2465-2497, XP002130647 ISSN: 0009-2665 das ganze Dokument ---	1-9,11, 13-33, 63-69
A	BALTZ R H ET AL: "Molecular genetic methods for improving secondary-metabolite production in actinomycetes" TRENDS IN BIOTECHNOLOGY,GB,ELSEVIER PUBLICATIONS, CAMBRIDGE, Bd. 14, Nr. 7, 1. Juli 1996 (1996-07-01), Seiten 245-250, XP004035763 ISSN: 0167-7799 das ganze Dokument ---	
P,X	WO 99 46387 A (BROUGHTON M CHRISTINE ;MADDURI KRISHNAMURTHY (US); WALDRON CLIVE () 16. September 1999 (1999-09-16) das ganze Dokument -----	1-9,11, 13-33, 63-69

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INTERNATIONALER RECHERCHENBERICHT

| Feld I | Bemerkungen zu den Ansprüchen, die sich als nicht recherchierbar erwiesen haben (Fortsetzung von Punkt 2 auf Blatt 1) |

Gemäß Artikel 17(2)a) wurde aus folgenden Gründen für bestimmte Ansprüche kein Recherchenbericht erstellt:

1. ☐ Ansprüche Nr.
weil sie sich auf Gegenstände beziehen, zu deren Recherche die Behörde nicht verpflichtet ist, nämlich

2. ☐ Ansprüche Nr.
weil sie sich auf Teile der internationalen Anmeldung beziehen, die den vorgeschriebenen Anforderungen so wenig entsprechen, daß eine sinnvolle internationale Recherche nicht durchgeführt werden kann, nämlich

3. ☐ Ansprüche Nr.
weil es sich dabei um abhängige Ansprüche handelt, die nicht entsprechend Satz 2 und 3 der Regel 6.4 a) abgefaßt sind.

| Feld II | Bemerkungen bei mangelnder Einheitlichkeit der Erfindung (Fortsetzung von Punkt 3 auf Blatt 1) |

Die internationale Recherchenbehörde hat festgestellt, daß diese internationale Anmeldung mehrere Erfindungen enthält:

1. ☐ Da der Anmelder alle erforderlichen zusätzlichen Recherchengebühren rechtzeitig entrichtet hat, erstreckt sich dieser internationale Recherchenbericht auf alle recherchierbaren Ansprüche.

2. ☐ Da für alle recherchierbaren Ansprüche die Recherche ohne einen Arbeitsaufwand durchgeführt werden konnte, der eine zusätzliche Recherchengebühr gerechtfertigt hätte, hat die Behörde nicht zur Zahlung einer solchen Gebühr aufgefordert.

3. ☐ Da der Anmelder nur einige der erforderlichen zusätzlichen Recherchengebühren rechtzeitig entrichtet hat, erstreckt sich dieser internationale Recherchenbericht nur auf die Ansprüche, für die Gebühren entrichtet worden sind, nämlich auf die Ansprüche Nr.

4. ☒ Der Anmelder hat die erforderlichen zusätzlichen Recherchengebühren nicht rechtzeitig entrichtet. Der internationale Recherchenbericht beschränkt sich daher auf die in den Ansprüchen zuerst erwähnte Erfindung; diese ist in folgenden Ansprüchen erfaßt:
1-9, 11, 13-33, 63-69 alle partiell

Bemerkungen hinsichtlich eines Widerspruchs
☐ Die zusätzlichen Gebühren wurden vom Anmelder unter Widerspruch gezahlt.

☐ Die Zahlung zusätzlicher Recherchengebühren erfolgte ohne Widerspruch.

WEITERE ANGABEN PCT/ISA/ 210

1. Ansprüche: 1-9, 11, 13-33, 63-69 (alle partiell)

   Nucleinsäure gemäss SEQ ID NO:7, davon ableitbares
   Genprodukt, Vektor umfassend zumindestens die Nukleinsäure
   gemäss SEQ ID NO:7, Wirtszelle enthaltend eine Nucleinsäure
   gemäss SEQ ID NO:7, Antikörper welcher spezifisch mit dem
   Genprodukt reagiert und Verfahren zur Herstellung der
   Nucleinsäure, des Polypeptides oder Spinosyns.

2. Ansprüche: 1-9, 11, 13-31, 34, 35, 63-69 (alle partiell)

   Wie Erfindung 1 aber für Nucleinsäure gemäss SEQ ID NO:9,
   davon ableitbares Genprodukt und Gegenstände welche sich
   darauf beziehen.

3. Ansprüche: 1-72 (alle partiell und sofern zutreffend) -
          24. Ansprüche: 1-
          72 (alle partiell und sofern zutreffend)

   Wie Erfindung 1 aber für Nucleinsäure gemäss SEQ ID NO:11
   bis SEQ ID NO:54, davon ableitbare Genprodukte und
   Gegenstände welche sich darauf beziehen.

INTERNATIONALER RECHERCHENBERICHT

Angaben zu Veröffentlichung..., die zur selben Patentfamilie gehören

Im Recherchenbericht angeführtes Patentdokument	Datum der Veröffentlichung	Mitglied(er) der Patentfamilie		Datum der Veröffentlichung
WO 9946387 A	16-09-1999	US	6143526 A	07-11-2000
		AU	2680099 A	27-09-1999
		BR	9909257 A	28-11-2000
		EP	1062345 A	27-12-2000